### SEQUENCE LISTING

(1) INFORMATION FOR SEQ ID NO: 1:

(i)SEQUENCE CHARACTERISTICS:

(A)LENGTH: 6 amino acids

(B) TYPE: amino acid

(D)TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v)FRAGMENT TYPE: internal fragment

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Asn Asp Gln Val Leu Phe 1 5

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A)LENGTH: 6 amino acids

(B) TYPE: amino acid

(D)TOPOLOGY: linear

(ii) MOLECULE TYPE: internal fragment

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Phe Glu Asp Met Thr Asp 1 5

(3) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A)LENGTH: 7 amino acids

(B)TYPE: amino acid

(D)TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v)FRAGMENT TYPE: internal fragment

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Phe Lys Leu Ile Leu Lys Lys 1 5

(4) INFORMATION FOR SEQ ID NO: 4:

(i)SEQUENCE CHARACTERISTICS:

(A)LENGTH: 5 amino acids

(B)TYPE: amino acid

(D)TOPOLOGY: linear

(ii) MOLECULE TYPE: internal fragment



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Tyr Lys Asp Ser 1 5

- (5) INFORMATION FOR SEQ ID NO: 5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5 amino acids
    - (B) TYPE: amino acid
    - (D)TOPOLOGY: linear
  - (ii) MOLECULE TYPE: internal fragment
  - (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ser Thr Leu Ser Cys 1 5

- (6) INFORMATION FOR SEQ ID NO: 6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A)LENGTH: 157 amino acids
    - (B)TYPE: amino acid
    - (D)TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 6:
- Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn 10 15
- Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile 35 40 45
- Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile 50 55 60
- Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile 65 70 75 80
- Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys 85 90 95
- Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys 100 105 110
- Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu 115 120 125
- Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu 130 135 140
- Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp 145 150 155
- (7) INFORMATION FOR SEQ ID NO: 7:
  - (i)SEQUENCE CHARACTERISTICS: (A)LENGTH: 157 amino acids





(B)TYPE: amino acid
(D)TOPOLOGY: linear

# (ii) MOLECULE TYPE: peptide

# (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met 25 Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile 40 45 Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser 55 60 Val Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile 70 75 Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser 90 95 85 Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu 110 Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu 125 120 Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp 135 140 Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser 145 150

### (8) INFORMATION FOR SEQ ID NO: 8:

### (i) SEQUENCE CHARACTERISTICS:

- (A)LENGTH: 471 base pairs
- (B)TYPE: nucleic acid
- (C)STRANDEDNESS: double
- (D)TOPOLOGY: linear

### (ii) MOLECULE TYPE: cDNA

# (vi)ORIGINAL SOURCE:

- (A)ORGANISM: human
- (G)CELL TYPE: liver

### (ix)FEATURE:

- (A)NAME/KEY: mat peptide
- (B)LOCATION: 1..471
- (C)IDENTIFICATION METHOD: E

### (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TAC	TTT	GGC	AAG	CTT	GAA	TCT	AAA	TTA	TCA	GTC	ATA	AGA	AAT	TTG	AAT	48
Tyr	Phe	Gly	Lys	Leu	Glu	Ser	Lys	Leu	Ser	Val	Ile	Arg	Asn	Leu	Asn	
1				5					10					15		
GAC	CAA	GTT	CTC	TTC	ATT	GAC	CAA	GGA	AAT	CGG	CCT	CTA	TTT	GAA	GAT	96
Asp	Gln	Val	Leu	Phe	Ile	Asp	Gln	Gly	Asn	Arg	Pro	Leu	Phe	Glu	Asp	
			20					25					30			
ATG	ACT	GAT	TCT	GAC	TGT	AGA	GAT	AAT	GCA	CCC	CGG	ACC	ATA	TTT	ATT	144

Met	Thr	Asp 35	Ser	Asp	Cys	Arg	Asp 40	Asn	Ala	Pro	Arg	Thr 45	Ile	Phe	Ile	
ATA	AGT	ATG	TAT	AAA	GAT	AGC	CAG	CCT	AGA	GGT	ATG	GCT	GTA	ACT	ATC	192
Ile	Ser 50	Met	Tyr	Lys	Asp	Ser 55	Gln	Pro	Arg	Gly	Met 60	Ala	Val	Thr	Ile	
TCT	GTG	AAG	TGT	GAG	AAA	ATT	TCA	ACT	CTC	TCC	TGT	GAG	AAC	AAA	ATT	240
Ser 65	Val	Lys	Cys	Glu	Lys 70	Ile	Ser	Thr	Leu	Ser 75	Cys	Glu	Asn	Lys	Ile 80	
ATT	TCC	TTT	AAG	GAA	ATG	AAT	CCT	CCT	GAT	AAC	ATC	AAG	GAT	ACA	AAA	288
Ile	Ser	Phe	Lys	Glu 85	Met	Asn	Pro	Pro	Asp 90	Asn	Ile	Lys	Asp	Thr 95	Lys	
AGT	GAC	ATC	ATA	TTC	TTT	CAG	AGA	AGT	GTC	CCA	GGA	CAT	GAT	AAT	AAG	336
Ser	Asp	Ile	Ile 100	Phe	Phe	Gln	Arg	Ser 105	Val	Pro	Gly	His	Asp 110	Asn	Lys	
ATG	CAA	TTT	GAA	TCT	TCA	TCA	TAC	GAA	GGA	TAC	TTT	CTA	GCT	TGT	GAA	384
Met	Gln	Phe 115	Glu	Ser	Ser	Ser	Tyr 120	Glu	Gly	Tyr	Phe	Leu 125	Ala	Cys	Glu	
AAA	GAG	AGA	GAC	CTT	TTT	AAA	CTC	ATT	TTG	AAA	AAA	GAG	GAT	GAA	TTG	432
Lys	Glu 13	Arg 30	Asp	Leu	Phe	Lys 135	Leu	Ile	Leu	Lys	Lys 140	Glu	Asp	Glu	Leu	
GGG	GAT	AGA	TCT	ATA	ATG	TTC	ACT	GTT	CAA	AAC	GAA	GAC				471
_	Asp	Arg	Ser	Ile		Phe	Thr	Val	Gln		Glu	Asp				
145					150					155						

### (9) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A)LENGTH: 11 amino acids
  - (B)TYPE: amino acid
    (D)TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v)FRAGMENT TYPE: N-terminal fragment
- (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser 1 5 10

- (10) INFORMATION FOR SEQ ID NO: 10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A)LENGTH: 10 amino acids
    - (B)TYPE: amino acid
    - (D)TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (v)FRAGMENT TYPE: C-terminal fragment
  - (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Ser Ile Met Phe Thr Val Gln Asn Glu Asp 1 5 10



- (11) INFORMATION FOR SEQ ID NO: 11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A)LENGTH: 13 amino acids
    - (B)TYPE: amino acid
    - (D)TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (v)FRAGMENT TYPE: N-terminal fragment
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg 1 5 10

- (12) INFORMATION FOR SEQ ID NO: 12:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A)LENGTH: 14 amino acids
    - (B) TYPE: amino acid
    - (D)TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (v)FRAGMENT TYPE: internal fragment
  - (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg
1 5 10

- (13) INFORMATION FOR SEQ ID NO; 13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A)LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (D)TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (v)FRAGMENT TYPE: internal fragment
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys 1 5 10 15

- (14) INFORMATION FOR SEQ ID NO: 14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A)LENGTH: 471 base pairs
    - (B) TYPE: nucleic acid
    - (C)STRANDEDNESS: double
    - (D)TOPOLOGY: linear



### (ii) MOLECULE TYPE: cDNA

### (ix)FEATURE:

(A)NAME/KEY: mat peptide

(B)LOCATION: 1..471

(C)IDENTIFICATION METHOD: S

# (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TAC Tyr	TTT Phe	GGC Gly	AAG Lys	CTT Leu 5	GAA Glu	TCT Ser	AAA Lys	TTA Leu	TCA Ser 10	GTC Val	ATA Ile	AGA Arg	AAT Asn	TTG Leu 15	AAT Asn	48
GAC Asp	CAA Gln	GTT Val	CTC Leu 20	TTC Phe	ATT Ile	GAC Asp	CAA Gln	GGA Gly 25	AAT Asn	CGG Arg	CCT Pro	CTA Leu	TTT Phe 30	GAA Glu	GAT Asp	96
ATG Met	ACT Thr	GAT Asp 35	TCT Ser	GAC Asp	TCT Ser	AGA Arg	GAT Asp 40	AAT Asn	GCA Ala	CCC Pro	CGG Arg	ACC Thr 45	ATA Ile	TTT Phe	ATT Ile	144
ATA Ile	AGT Ser 50	ATG	TAT Tyr	AAA Lys	GAT Asp	AGC Ser 55	CAG Gln	CCT Pro	AGA Arg	GGT Gly	ATG Met 60	GCT Ala	GTA Val	ACT Thr	ATC Ile	192
TCT Ser 65	GTG	AAG Lys	TCT Ser	GAG Glu	AAA Lys 70	ATT	TCA Ser	ACT Thr	CTC Leu	TCC Ser 75	GCT Ala	GAG Glu	AAC Asn	AAA Lys	ATT Ile 80	240
ATT	TCC Ser	TTT Phe	AAG Lys	GAA Glu 85	ATG	AAT Asn	CCT Pro	CCT Pro	GAT Asp 90	AAC Asn	ATC Ile	AAG Lys	GAT Asp	ACA Thr 95	AAA Lys	288
AGT Ser	GAC Asp	ATC Ile	ATA Ile 100	TTC	TTT Phe	CAG Gln	AGA Arg	AGT Ser 105	GTC	CCA Pro	GGA Gly	CAT His	GAT Asp 110	AAT Asn	AAG Lys	336
ATG Met	CAA Gln	TTT Phe 115	GAA	TCT Ser	TCA Ser	TCA Ser	TAC Tyr 120	GAA	GGA Gly	TAC Tyr	TTT Phe	CTA Leu 125	GCT Ala	TGT Cys	GAA Glu	384
AAA Lys	GAG Glu 130	AGA	GAC Asp	CTT Leu	TTT Phe	AAA Lys 135	CTC	ATT Ile	TTG Leu	AAA Lys	AAA Lys 140	GAG	GAT Asp	GAA Glu	TTG Leu	432
	GAT					TTC					GAA Glu					471

### (15) INFORMATION FOR SEQ ID NO: 15:

### (i) SEQUENCE CHARACTERISTICS:

- (A)LENGTH: 10 amino acids
- (B)TYPE: amino acid
- (D)TOPOLOGY: linear

# (ii)MOLECULE TYPE: peptide

- (v)FRAGMENT TYPE: N-terminal fragment
- (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser 1 5



# (16) INFORMATION FOR SEQ ID NO: 16:

# (i) SEQUENCE CHARACTERISTICS:

- (A)LENGTH: 471 base pairs
- (B)TYPE: nucleic acid
- (C)STRANDEDNESS: double
- (D)TOPOLOGY: linear

# (ii) MOLECULE TYPE: cDNA

### (ix)FEATURE:

- (A)NAME/KEY: mat peptide (B)LOCATION: 1..471
- (C)IDENTIFICATION METHOD: S

# (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 16:

			GAA Glu							48
			ATT Ile							96
			TCT Ser							144
			GAT Asp							192
			AAA Lys 70							240
			ATG Met							288
		TTC	TTT Phe							336
			TCA Ser							384
	AGA		TTT Phe		CTC					432
GAT			ATG Met 150	TTC			GAA			471

# (17) INFORMATION FOR SEQ ID NO: 17:

### (i) SEQUENCE CHARACTERISTICS:

- (A)LENGTH: 11464 base pairs
- (B)TYPE: nucleic acid
- (C)STRANDEDNESS: double
- (D)TOPOLOGY: linear



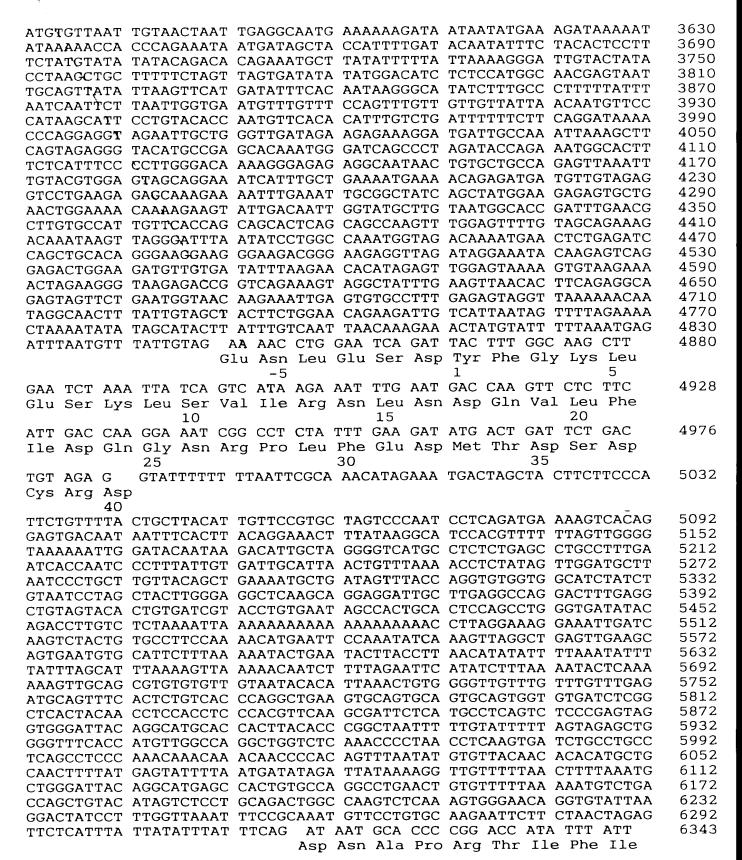
(ii) MOLECULE TYPE: genomic DNA

(vi) ORIGINAL SOURCE: (A)ORGANISM: human (G)CELL TYPE: placenta (ix)FEATURE: (A)NAME/KEY: 5 UTR (B)LOCATION: 1..3 (C) IDENTIFICATION METHOD: E (A)NAME/KEY: leader peptide (B)LOCATION: 4..82 (C)IDENTIFICATION METHOD: S (A)NAME/KEY: intron (B)LOCATION: 83..1453 (C)IDENTIFICATION METHOD: E (A)NAME/KEY: leader peptide (B)LOCATION: 1454..1465 (C) IDENTIFICATION METHOD: S (A)NAME/KEY: intron (B)LOCATION: 1466..4848 (C)IDENTIFICATION METHOD: E (A)NAME/KEY: leader peptide (B)LOCATION: 4849..4865 (C)IDENTIFICATION METHOD: S (A)NAME/KEY: mat peptide (B)LOCATION: 4866..4983 (C) IDENTIFICATION METHOD: S (A)NAME/KEY: intron (B)LOCATION: 4984...6317 (C) IDENTIFICATION METHOD: E (A)NAME/KEY: mat peptide (B)LOCATION: 6318..6451 (C)IDENTIFICATION METHOD: S (A)NAME/KEY: intron (B)LOCATION: 6452..11224 (C)IDENTIFICATION METHOD: E (A)NAME/KEY: mat peptide (B)LOCATION: 11225..11443 (C) IDENTIFICATION METHOD: S (A)NAME/KEY: 3° UTR (B)LOCATION: 11444..11464 (C) IDENTIFICATION METHOD: E (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 17: AAG ATG GCT GCT GAA CCA GTA GAA GAC AAT TGC ATC AAC TTT GTG GCA 48 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala -25 -30 -3598 ATG AAA TTT ATT GAC AAT ACG CTT TAC TTT ATA G GTAAGG CTAATGCCAT Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala -20 -15 -10 AGAACAAATA CCAGGTTCAG ATAAATCTAT TCAATTAGAA AAGATGTTGT GAGGTGAACT 158 ATTAAGTGAC TCTTTGTGTC ACCAAATTTC ACTGTAATAT TAATGGCTCT TAAAAAAATA 218 GTGGACCTCT AGAAATTAAC CACAACATGT CCAAGGTCTC AGCACCTTGT CACACCACGT 278 GTCCTGGCAC TTTAATCAGC AGTAGCTCAC TCTCCAGTTG GCAGTAAGTG CACATCATGA

338

AAATCCCAGT TTTCATGGGA A	AAATCCCAGT	TTTCATTGGA	TTTCCATGGG	AAAAATCCCA	398
GTACAAAACT GGGTGCATTC A	AGGAAATACA	ATTTCCCAAA	GCAAATTGGC	AAATTATGTA	458
AGAGATTCTC TAAATTTAGA G			TTATGTAAAT	ATGTTTGACA	518
AGTAAAAATT GATTCTTTTT I	րդարարարա				578
CTCTGCTCAC TGCAACCTCC A	ACCTCCTGGG	TTCAAGCAAT	TCTCCTGCCT	CAGCCTTCTG	638
AGTAGCTGGG ACTACAGGTG				ATTTTTACTA	698
GAGACAGGGT TTTGGCATGT I	PGTCCAGGCT	GGTCTTGGAC	TCCTGATCTC		758
CCTGCTCGG GCTCCCAAAG T	rCCTCCCATT	ACAGGCATGA	ACCACCACAC	ATGGCCTAAA	818
AATTGATTCT TATGATTAAT C			TCATTTGAAA	GTTTGCCTTC	878
ATTTGAAACC TTCATTTAAA A	ACCCTGIGAA	ACABACTCAC			938
TGCAAAATAT CCTGTGGACA	CTCTCCTACCT	TCTCTCCACC	CTGAAGCAGG	AGGATCACTT	998
GAGCCTAGGA ATTTGAGCCT G	CACTCACCT	ATCATCCCAC	CCCTACACTC	CAGCCTGCAT	1058
GACAGTAGAC CCTGACACAC A	ACACACAAAA	AAAAACCTTC	ΤΤΑΔΑΔΑΤΤ	ATTAGTTGAC	1118
TTTTCTTAGG TGACTTTCCG T		ΑΛΑΛΑΘΟΙΙΟ	CTAAAAATT	πααππππασα	1178
AAATTTATTT TTAGTTACAT A		MANTITUDAN	CCTTTAACTT	ππαπαπαπαπα α	1238
ATTACTGAG AACACACTAA		CUMCAMMONTA	TEGECETTTT	CCATCATTAT	1298
ATTACCTGAG AACACACTAA G	AACACACACC	CTICATITIA	AAAAATACCA	CTTCCACAAA	1358
GAGGAGTAGC AAAAGTAAAA G					1418
			GAA GAT GAT	G GTAAA	1470
TACATATTCT GTTTCTCTCT T	TTTTCCCCCT				14/0
		-10	Glu Asp As	p Giu	
	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		CHHCACACAC	$\lambda$ m C m $\lambda$ m C m C $\lambda$	1530
GTAGAAATGA ATTTATTTTT C	TTTGCAAAC	TAAGTATCTG	ACCA A MCMCC	CUMCANACAN	1590
CCATTGTCAG CTGAGGAAAA A	AAAAAAATGG	TTCTCATGCT	ACCAATCTGC	AAACAACAAC	1650
ATGTGGACTC AGTAGCACAG	CTTTGGAATG	AAGATGATCA	TAAGAGATAC	AAAGAAGAAC	1710
CTCTAGCAAA AGATGCTTCT C	CTATGCCTTA	AAAAATTCTC	ACCOMMISSION	MCMCMMCMAC	1710
ATAGACTTTG CCTGTTTCAT I	rggreetaag	ATTAGCATGA	AGCCATGGAT	TCTGTTGTAG	
GGGGAGCGTT GCATAGGAAA A	AAGGGATTGA	AGCATTAGAA	TTGTCCAAAA	CTCAGTAACAC	1830 1890
CTCCTCTCAG AAATGCTTTG	GGAAGAAGCC	TGGAAGGTTC	CGGGTTGGTG	CACAMMCACA	1950
GCAGAAAATT CTGGAAGTAG A					2010
GGCCAAAAGC TGAAAGAAAC C					2010
GTAGAGTAGG AGTAGGAGAC T					2130
GACGTTCTCT CACCCCAAGA T					
TAAGCACAAT ATGTATTAGC I			TGTAACAAAG		2190
ATACAGTAGC TGAATAAGAT A			AAAGTCTAAG		2250
AGAAGTAGTA TGGCTGGAAG					2310
GTACCCATCA TCCCCTAGTT G			TGAAAATCAT		2370
GGGTTCATAT CCCAGTTATC A	AAGAAAGGGT	CAAGAGAAGT	CAGGCTCATT		2430
ACTCTAATTG GAAGTTAAAC A	ACATCAATCC	CCCTCATATT	CCATTGACTA	GAATTTAATC	2490
ACATGGCCAC ACCAAGTGCA A					2550
ATGACTCTTT AAAATTCAGA A	AATAATATAT	TTTTAAAATA	TCATTCTGGC	TTTGGTATAA	2610
AGAATTGATG GTGTGGGGTG A	AGGAGGCCAA	AATTAAGGGT	TGAGAGCCTA	TTATTTTAGT	2670
TATTACAAGA AATGATGGTG T	rcatgaatta -	AGGTAGACAT	AGGGGAGTGC	TGATGAGGAG	2730
CTGTGAATGG ATTTTAGAAA C	CACTTGAGAG	AATCAATAGG	ACATGATTTA	GGGTTGGATT	2790
TGGAAAGGAG AAGAAAGTAG A	AAAAGATGAT	GCCTACATTT	TTCACTTAGG	CAATTTGTAC	2850
CATTCAGTGA AATAGGGAAC A	ACAGGAGGAA	GAGCAGGTTT	TGGTGTATAC	AAAGAGGAGG	2910
ATGGATGACG CATTTCGTTT I	rggatctgag	ATGTCTGTGG	AACGTCCTAG	TGGAGATGTC	2970
CACAAACTCT TCTACATGTG G	GTTCTGAGTT	CAGGACACAG	ATTTGGGCTG	GAGATAGAGA	3030
TATTGTAGGC TTATACATAG A	AAATGGCATT	TGAATCTATA	GAGATAAAAA	GACACATCAG	3090
AGGAAATGTG TAAAGTGAGA	GAGGAAAAGC	CAAGTACTGT	GCTGGGGGGA	ATACCTACAT	3150
TTAAAGGATG CAGTAGAAAG A	AAGCTAATAA	ACAACAGAGA	GCAGACTAAC	CAAAAGGGGA	3210
GAAGAAAAC CAAGAGAATT C	CCACCGACTC	CCAGGAGAGC	ATTTCAAGAT	TGAGGGGATA	3270
GGTGTTGTGT TGAATTTTGC A					3330
AGCAACAAGG AGTTTGGTGA I	rctcagtgaa	AGCAGCTTGA	TGGTGAAATG	GAGGCAGAGG	3390
CAGATTGCAA TGAGTGAAAC A	AGTGAATGGG	AAGTGAAGAA	ATGATACAGA	TAATTCTTGC	3450
TAAAAGCTTG GCTGTTAAAA	GGAGGAGAGA	AACAAGACTA	GCTGCAAAGT	GAGATTGGGT	3510
TGATGGAGCA GTTTTAAATC T	rcaaaataaa	GAGCTTTGTG	CTTTTTTGAT	TATGAAAATA	3570





ATA AGT ATG TAT ANA GAT AGC CAG CCT AGA GGT ATG GCT ACT ACT ATC 11e Ser Met Tyr Lys Asp Ser Gin Pro Arg Gly Met Alo Val Thr Ile 50 TCT GTG AAG TGT GAG AAA ATT TCA ACT CTC TCC TGT GAG AAC AAA ATT Ser Val Lys Cys Glu Lys 11e Ser Thr Leu Ser Cys Glu Asn Lys Ile 65 TCT GTG AAG GTAG GAG AAS ATT TCC TTT AAG GTAAG ACTGAGCCTT ACTTTGTTT CAATCAGTT AATATAATCA LIe Ser Phe Lys ATATAATTAG AAATATAACA TTATTTCTAA TGTTAATATA ACTGAGTAGAACT CAAAATTAGA CAAGCAACC TTTTGTCTAG AACAGAAATA ACAAGAAGCA GAGAACCATT CAAAATTAGAT CTTACTAAAA TATATAACAA TCTTTTACTAT TTTGTGATAAT GATGAGAACT CAAAATTAGAT CTTACTAAAA TATATAATATAAAC TCTTTACTAT TTTGTGATAAT ACAGTGATTT CTGAGCCTG CACAGGGGAA GAGGAGATAC ACACTTGTT TTATACAAC TCTTTTACTACT TTTGTGATAAT ACACTTCTAT TAATCTAAAT CATTTTAGAAT TATATATAAAC TCTTTAACTACT TTTATACCCT TTTTATACAAC TCTTTTAACTACA TATTTATATCT CTGAGCCTG CTCTAGAAA TAATAATATTAAAC TCTTTAACTAC TATTTATATCT CTGAGCCTG CTCTTCAGAA TAGAGTAAATA TATATACACA TCTTTAACTACAA TATTTATATCT CTTAGCCTAA GTCTTTAGAAA TATATATATCAAC TCTTTAAACTAC ACACTTGTT TATTTAACCC TAGTTTATTTC TCTCAGAAT TAGAGTAAAT TATATATCTC CATTGCATAA GACTTAAAAAT TATCAAATATA TTTATATCCT CTAGCCTAA GTCTTAGAAAT TATATATTC TGGCCTATA GACCAGGATA AAACTTTCT TCTCAGAATAA TATATATCTC CAACAGGCTAT AAAACTATTC TGGCCTCTAC CTTTATTGTTATATCC TAGTTGTTTT TCTTCATTTC TCTCATTTT TCTCATATTTATATCC TCAACTACAATTA AAATATACC CCTTTCAAACAACTAC CACACTTAAA ATTAATACAC AGCACTTATT TATTCACTA TTATTATATCC CAACCAGGTAT AAACTATCC TGAGAACACAC TTATTAATCCA AGCACAGATAA AACTAGACTA ATTAATACCA AAATCACACACATATA AAATAATACC CCACCCAC						
ILE SET MET TYP LYS ASP SER GIN PRO ATG GLY MET AND VAL THE 18 50 TOT GTG GAG AAA ATT TCA ACT CTC TCC TGT GAG AAC AAA ATT GAG ACT CTC GTG GAG AAC AAA ATT GAG ACT CTC TCC TGT GAG AAC AAA ATT GAG GAG ACT CTC GTG GAG AAC AAA ATT GAG GAG ATT CTC TCC TGT GAG AAC AAA ATT GAG GAG ACT AACT CTC CTC TGT GAG AAC AAA ATT GAG ACT CTC TCC TGT GAG AAC AAA ATT GAG ACT CTC TCC TGT GAG ACT ACT TCC TGT AACT CTC TCC TGT AACT CTC TCC TGT AACT CTC TCC TGT AACT CTC TCC TGT AACACT CTTT TCT AACT TCC AGACCAAC TTTTGTCTAG AACACAATT ACT AACACTAT ACT AACACT CTC CAGACCACC TTTTGTCTAG AACACAATT ACAACACT CTTTTACTAA TTTACTAA TTTACAAAA ATTATCAAAA ATTATCAAAA ATTATCAAAA ATTATCACAAC CTCTTACTACAAC TCCTTACCTAA TGTGATAAT GAGGAGACCA GAGGAGACCA TAACACTCCAGAA TGAGTTCTG TAACACACTAG CTCTTCAGAAA ACACACTTCTA TTTATCACAA TAACACTACT CTTTATCACAA TAATAATGTA GAACACACTAT TTTTATACACAA TAATAAATAAT ATTATACCA TATCACAACT TTTTTATACACAA TAATAACACAC TCCTTACAATT ACACACTACAA TAATAACACA CTCTTACACACAA TAATAACACACAACACAACACAACAACACAACACAACAAC		40		45		
50 Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Ash Lys Ile 50 ATT TCC TIT AAG GTAGA ACT ATTTCA ACT CTC TCT TGT GAG AAC AAA ATT 649 ATTTATATTAG AAATATAACA TLE SER PHE Lys ATATAATTAG AAATATAACA TTATTCTTTAT TGTCTAG AACAGAAATA ACAGAAATA ACAGAAATA CAAATATCAC CAGACACC TITTGTCTAGA ACAGAAATA ACAGAAATA ACAGAAATA ACAGAATAA ACAGAAATA ACAGAATACA TAAGAAAAAAAAAA	ATA AGT ATG TAT AAA	GAT AGC CAG	CCT AGA GGT	ATG GCT GTA	ACT ATC	6391
SET VAI LYS CYS GIU LYS ILS SET THE LEU SET CYS GIU ASN LYS ILE 55 70 80  ATT TCC TTT ANG GTAG ACTGAGCCTT ACTTGTTT CAATCAGTT AATATAATCA 16 96  ATT TCC TTT ANG GTAG ACTGAGCCTT ACTTGTTT CAATCAGTT AATATAATCA 16 97  ATATTAATTAG AAATATAACA TTATTAATTAG AAATATAACA TTATTAATTAG AAATATAACA TTATTAATTAG AAATATAACA TTATTACAAAA ATTATCAAAA TGTTAATATA AGAAGAGCA GAGAACCATT AAAGTGAATA CTTACTAAAAA ATTATCAAAC TCTTTACCTA TGTGATAAT GAGAGACCAGTT AAAGTGAATA CTTACTAAAA ATTATCAAAC TCTTTACCTA TGTGAGTAAT GAGAGACCAGTT ACAATCAGCT TTATACAAA ATTATCAAAC TCTTTACCTA TTGTGATAAT GAGAGTTTTT CAGACCAGCT CACACGGAA GAGGAGATAC AAACACTTGTT TTATGAGCTG CATCTCCTGA ACAATCAGCT CTTACTAAAA ATTATAATGAGA ATAACATTAT GTGAGTTATA CATTTAAGAA TAACATCAGT TTTATACAAA TAATAATATATATCCT ATTGTGATAAT TACCTATAACAACTACT TTTATACAAA TAATAATATATAT	Ile Ser Met Tyr Lys		Pro Arg Gly		l Thr Ile	
SET VAI LYS CYS GIU LYS 11e SET THE LEU SET CYS GIU ASN LYS 11e 65 70 75 5 80 80 80 80 80 80 80 80 80 80 80 80 80						
ATT TCC TTT AAG GTAAG ACTGAGCCT ACTTGTTT CAATCATCT ACTATAATCA 6496 Ile Ser Phe Lys ATATAATTAG ANATATAACA TTATTTCTAA TGTAATATA AGTAATGTA ATAGAAAACT 6556 CAAATATCT CAGACCAACC TTTTGTCTAG AACAGAAATA ACAAGAAGCA GAGAACCATT 6616 AAAGTGAATA CTTACTAAAA ATTATCAAAA CTTTTACTAA TTGTGATAAT GAGATCATT 6676 CCAAACAATCAGC TTTACAAA ATATATCAAAC TCTTTACCTAA TTGTGATAAT GATGGTTTTT 66736 ACAATCAGCT TTTATACAAA TAATAATGTA GAGACATCT TTAGGATTATA CATTTACAAA TAATAATGTA GAGATCATG TTTAGGATTATA CATTTACAAA TAATAATGTA GAGATCATGT TTATGTGATTATA CATTTACAAA TAATAATGTA GAGATCATGT TTATGTGATATAT GAGATTATA CATTTACAAA TAATAATGTA GAGATCATGT TTATGTGATATT GTGAGTTATA CATTTACAAA TAATAATGTA GAGATCATGT TTATGTGATAAT GAGATTATA CATTTACAAA TAATAATGTA GAGATCAATT GTGAGTTATA CATTTAAGAAA CAACCTTCAG TTATGAGAAAT AAACATTAT GTGAGTTATA CATTTAAAAAAGT TATGAGAAAATA TATGATAAAAA GAACCTTCAG CTTTACAAAA TAATAATATT TAATACCC TTAGGAGTAATT ATCTTCAAAAATT GAATAAAAAGT TAATGAGAAAAA TAATAAAAAGT TAATGATAAAA TAATAATCAC CTTTAGAAC CAAGACCTCAAG CTTTCAGATGT ATGTGATAATT TAATCCTCA TAATACCTAC TAATACCTAA GACCAGGATA AAAAAAAAAA						6439
ATT TCC TTT AAG GTAAG ACTGAGCCTT ACTTGTTT CAATCATGTT AATATAATCA 11e Ser Phe Lys ATATAATATAG AAATATAACA TTATTTCTAA TGTTAATATA AGTAATGTAA TTAGAAAACT CAAAATATCA CACACCAACC TTTTGTCTAG AACAGAAGCA GAGAACCATT CTGAGCCTG CACAGGGGAA GAGGAGATAC ACCTTGTTCT TTATGACAAA GAGAGAGCA GAGAACCATT CTGAGCCTG CACAGGGGAA GAGGAGATAC ACCTTGTT TTATGACCTG CATCTCCTGA TAACATCAGTC TTTATACAAA ATATATGAAA CTTTTACCTA TTGTGATAAT GTACTTTTAGACA TAACATCAGTC TTTATACAAA TATATGAAA CACATCTGTT TATGACCTG CATCTCCTGA TAACATCAGTC CTTTCCAGAA TGAGTTCTGC TATGAGAGAACCAT TATTTCTACAC CTTTGTAAAT TATGATAATAT TTTTATACCCTG CATCTCTCTA TATTCTACAC CTTTGTAAAT TATGATAATAT TTTTATACCCTA TGTGATATA TATCCTTCTAT TATTCTACAC CTTTGTAAAT TATGAGATAC CACCTCTGAGT CAGCCAGCATATA ATATCTTCACA CTTTAGACA GTCTTAGACA CAAGCTTCAG CTTCCAGTTG ATGTATTTT TTCCTGATC TAATCTAATT GAATAAAAGT TATGAGAATCA GTCTCAGAGT ATATGTTTT TCCTCATCT TAATCTAATT TCCTCATTTC CTCCATTATT GTTAAAAATAT ATATCCTCA TATTATCTCC TAATTATTTT TCCTCATTTC CTCCATTATT GTTAAAATAT GGCAATTAA CTATTACTCC CTATTATTTT TCCTCATTTC CTCCATTATT GTTAAAATAT GGCAATTAA CTATTACTCC CTATTATTTT TCCTCATTTC CTCCATTATT GTTAAAATAT GGCAATTAAC GACCAGCCA GTAAAGAGACC CTTTGAAAAT GTAATGCTTA ATTATCTCC TTCCATGCA GAGCACCC CAGGGATAG GATTGACAATT GGCAATTAAC CCACCCAGC CAGCACAGAC AAACCCCTCA AATAAATACC AGTAAGACAC GCTTCAAAAAA CCTCACCAGAC CAAAAAAAA CCACCTCTAAA ATATAATCC AGTAAGACAC GCCCCCACCACC CCACCCAGC CACCACAAAAAAAAAA	Ser Val Lys Cys Glu	Lys Ile Ser	Thr Leu Ser	Cys Glu As		
ATATAMATAG AMATATAGA TTATTTCTAA TGTTAATATA AGTAATGTAA TTAGAAAACT 6556 CAAATATCCT CAGACCAACC TTTTGTCTAG AACAGAAATA ACAAGAAGCA GAGAACCAT 6616 AAAGTGAATA CTTACTAAAA ATTATCAAAC TCTTTACCTA TTGTGATAAT GATAATGTAAT GATAGATAAT CATACTAAAA ATTATCAAAC TCTTTACCTA TTGTGATAAT GATACTATT 6756 CTGAGCCTGT CACAGGGGAA GAGGAGTAC AACACTTGTT TTATGACCTG CATCTCTGA 6736 ACAATCAGTC TTTATACAAA TAATAATGTA GAATACATTT TTATGACCTG CATCTCTAA TAACATCAGC CTTTGAGATTATA CATTTACAAAA TAATAATGTA GAATACATTT TTATGACTAAT ATCTTCTAT 6856 ATTTCTACAC CTTTGTAAAA TAATAATGTA GAATACACATT TTATGACTAAT ATCCTTCTAT 6716 ATTTCTACAC CTTTGGAAAA TAATAATGTA TATTAATCCC TAGTGTTTT GTTCCTGAT 6717 TAATCTAATT GAATAAAAGT TATGAGAACA GCTCCAGTTG ATGTATGTA TTTTAATTCT 7036 AGCCAGGTAT AAAGAATTTC TGGCCCTACA TTTTTCTATT TATTTCTCA TATTATCTCT 7036 AGCCAGGTAT AAAGAATTTC TGGCCCTACA TTTTTCTATT TATTTCCA TTATTATTCT 7036 CAATTAATTTT TCTCTATTTC CTCCATTATT GTTAGATAAA CACAATTAA ATTATCTTC 7036 CAATTAATTTT TCTCTATTTC CTCCATTAGT GTTAGATAAA CACAATTAA CATTAGAGAAA 7166 CATTAGGTAA GACAGTTAGA GACAGTTAGA AATAACCCT AGAAGAACA 7166 CCACCCAGGC CCCACGGGAT GAAAAAAC CACAGGAAAAAA CACAATTAA CACAAATTAA CATAGAGAAA 7166 CCACCCAGCC CCCACCCAGAAAAAC CACAGGAGAA AATACCCT AGAAAAAAA CACAAATTAA CACAAATTAA CACAAATAA AATAAAATCCA AGCAAACACAAAAAAA CACAAAAAAAAAA						
ATATATTAG AÁTATAACA THATTICTAA TOTTAATATA AGTAATGTAA TTAGAAAACC 6616 CAAAATACCT CAGACGACC TTTTGTCTAG AACAGAATA ACAAGAGCA AGGAACCATT CACAGCGGA CACGGGAGA GAGGAGATAC ACACATTAT TTATGACTAC 6736 ACAATCACTC TATATACAAA TATATCAAAC TCTTTACCTA TTATGACATG CATCTCCTGA 6736 ACAATCACTC TTATATACAAA TAATAATGTA GAATACATAT TTATGACCTG CATCTCCTGA 6736 ACAATCACTC CTTATACAAA TAATAATGTA GAATACATAT TTATGACCTG CATCTCCTGA 6736 ACAATCACAC CTTTCAGAAA TAATAATGTA GAATACATAT TGAGACTTG CATCTCCTGA 6736 ATTCTCACAC CTTTGAAAT TATAGATAATT TTATAACCT TATGTTTTTT TTCTCATAT ACCTTCATAT TATGATAATAT TATTATATCC TATGTTTTT TTATGACATA TCCTTCATAT TAATACATAT TAATACATATA TATTATATCC TATGTTTTT TTATACCTATA TCCTTCATAT TAATACATAT TAATACATATA TATTATATACC TATTATATCTTCA AGCCAGATAT AACATATAC CACACATAAA CACATAAAC TATATACTTCA 7036 AGCCAGGTAT AACATATAC CACACGGATT CACCACACACA AGCACTAACA GACACAAAAA AACACATAAA CACACAATAAA CATATACCTAC 7156 AGACTAGACC AGTAAGACTA TTATGAGACA ACACATAAA CACACAATAAA CATATACCTAC 7156 AGACTAGACC AGTAAGACTA TTATGAGAGA ATATACCTC ATATATATCTC 7036 ACACACACACAC CACACTAGAA GACACTAGAG ATATACACTC AACACATAAA CACACATACA CACACATACA CACACATACA CACACATACA CACACATACA CACACATACA CACACACA	ATT TCC TTT AAG GTA	AG ACTGAGCCTT	ACTTTGTTTT	CAATCATGTT	AATATAATCA	6496
CARATATCCT CAGACCAACC TITTGTCTAG AACAGAANTA ACAAGAAGCA GAGAACCATT CTGAGCCTGT CACAGGGGAA GAGAGATA CTATTACCTA TGTGTGATAAT GAGTGTTTT CTGAGCCTGT CACAGGGGAA GAGAGATAC AACACTTGTT TATGACCTG CATCTCTGA CAATCACTC TITTATACAAA TAATAATGTA GAATACATAT GTGAGTTATA CATTTAAGAC ACAATCACTC TITTATACAAA TAATAATGTA GAATACATAT GTGAGTTATA CATTTAAGAC CTTTGCACAAA TAAGAATATAT TATGATAATA TATGATATAT TATGATATAT ATCCTTCTAT AACACTGTAA GTCTTAGACA CAAGCTTCAG CTTCCAGTTA AGATGTATT TTTTAATCCT CTTAGACCTAAA TAATAAAAT TATGATAATAT TTTTAATCCC TAGTTGTTTT GTGCTGAACC AGACCAAGTTA AACATATTC TGGCCCCTAC CTTCCAGTTC ATGATGTTA TTTTTAATCTCA CACCAGGTAT AAAGTATTC TGGCCCCTAC CTTCCAGTTC ATGATGTTA TTTTTAATCTCA CACCAGGTAT AAAGTATTC TGGCCCCTAC CTTCTACTAATTTTCTCCA TTATATATCTC CACCACGTC CCACTGAAA GACACTTTTTTTGTAGACA CAAAAAAAATACC GCTTCCAAGCACAA GACACATTAGA GAATACATTA CTCACACACAAGACCCA CACCACAAAAAAAAAA						
AAGGTGAATA CTTACTAAAA ATTATCAAC TCTTTACCTA TGTGATAAT GATGGTTTTT CTGAGCGTGT CACAGGGGAA GAGGAGATA AACACTTGTT TATGACCTG CATCTCCTGA 6736 ACAATCACTC TTATACAAA TAATAATGTA GAATACTAT TTATGACCTG CATCTCCTGA 6736 TAACCATGAC CTTTCAGAAA TAATAATGTA GAATACATAT GTGAGTTATA CATTTAAGAA ATTCTCACAC CTTTGAAAT TATGATAATAT TTATAATCC TAGTGTTTTTTTATAGAA ATTCTCACAC CTTTGAAAT TATGATAATAT TTATAATCC TAGTGTTTTTTTATATCACAT CTAACCTAAA GTCTTAGACA CAAGCTTCAG CTTCCAGTTG AGAGCTAATT ATCCTTCATT CATATCTAATT GAATAAAAGT TATGAGAATCA GTGCTAAAAC TAATGCTATA ATTATCTTCA AGCCAGGTAT AAAGTATTC GTGCCTCAC TTTTTCTCA TTATTCTCA TATTATCTTCA AGCCAGGTAT AAAGTATTC CTCCATTATT GTTAGAAAAA TAATGCTATA ATTATCTCA AGCCAGGTAT AAAGTATTC CTCCATTATT GTTAGAAAAA CACAATTAA CTATATCTCA AGCCAGGCAGTAT AAAGTATTC CTCCATTATT GTTAGAAAAA CACAATTAA CTATATCTCA AGCCAGGCAC AGTAAGACTA TTTTGAGTGG AGATTGCCA ATAAAATATCC CTATTATCTCA AGACTAGACA GCCCCAGAC AAATCACCTCA AAACAATAAA CACAAATAA CACAAATAA CACAAATAA CACAATAAA CACAAATAAA CACAAAAAAAA						
CEGAGCCTOT CACAGGGGAA GAGGAGATAC AACACTTGTT TTATGACCTG CATTCACGA (6736 ACAATCAGTC TITATACAAA TAATAATCA GAATACATA GAGGAGTATA ATCCTTCAT AACATGGA CTTTCCAGAA TGAGTTCTCC TATGAGAAT GAAGCTAATT ATCCTCTAT CTTAGCCA CTTTGTAGACA CAAGCTTCAG CTTCAGCTCA TATTAGAAT TATGATATA TTTTAATCCC TAGTCATATT GAATACAAT TATGAGATCA GCTGCAGTTGA TATTTTAATCTC TAATCTAATT GAATAAAAGT TATGAGATCA GCTGCAGTTGA TATTTTTAATCTC 7036 AGCCAGGTAT AAAGTATTCT TGGCCTCTAG CTTCTCATATA ATTATCTCACA TTTTTTAATTTT TTTTAATTTT 7096 CTATTATTTT TCTCTATTTC CTCCATTATT GTTGCTATA ATTATCTCCA TATTTTATTT						
ACARTCAGTC TITATACCAA TAATHATGTA GAATACATAT GTGAGTTTA CATTIAAGAA (6796) TAACARGTGA CITTCCAGAA TGAGGTCTCC TATGAGAAT GAGCTAANT ATCCTTCTAT (6856) ATTTCTACAC CITTGTAAAT TATGATAATA TTTTAATCC TAGTTGTTT GTGCCTAAT GATTACCCTAAG GTCTTAGGAC CAAGCTCAG CITCCAGTTG ATGTATGTTA TTTTTAATCT (6976) TAATCTAAT GAATAAAAGT TATGAGATAC GCTGTAAAAG TAATGCTATAA TTATTATTCT (7036) AGCCAGGTAT AAAGAGTT ATGAGATAC GCTGTAAAAG TAATGCTATAA TTATTATTCT (7056) AGACTGAGCC AGTAAGAGTA GCCCCTCTAC TITTTCCTCA TTATTCTCA TTATTATTCT (7096) CTATTATTTT TCTCATTTC CTCCATTATT GTAGAGATAA CCACAATTAA CATTAAGCTAC (7156) AGACTGAGC AGTAAGAGTA GCCAGGGAT GCCAGAGTAA CACAATTAA CATTATCTCA (7096) CTCACCCAGC CCACCACAATAAG GACAGTTAAGG ATTTGCCA ATAAATATCC GCTTTCATCC (7276) CCACCCAGT CCACCAGAAA AAACCCCTC AGAATGACCA CCACCACAATAAC CCACCACAATAAA ATATAATCCA AGTAGAGACCA (7366) ACTTGGTAGG GAGAAAAAG CCACCTCTAAA ATATAATCCA AGTAGAACAA GTGCCACCCC (7456) TCAGGTGAC AATTTGGAGT CCCCATACA ATATAACACA AGTAGAACAA GTGCCACCCC (7456) CCATAAGAGG CCTGGGATGG AAGGGTAGGG TGGAAAAGGT TAGTGCACACCC (7456) CCACCAGAC AAATCCA CCCCCAGAC AAACCCACTACA GCACAATGCC TAGAACATA TATCAAAATA (7516) CCATAAGAGG CCTGGGATGG AAGGGTAGGA GCCCAACCAG GCAGCTTAGT TATCAAAATA (7516) CCATAAGAGG CCTGGGATGG AACCTGGGAT AACCTGAACAT ATTTGGGAATAG AGCAATACCA (7576) AGCTGCAGACG GCAGATTCAG AAACTGGGAT AACTGGGAT AACCTGAACAT ATTTGGGAAAAGG TAGAGAAAACAT ATTTGGAGAACCA GCCAAAAAGCAT ATTTGGGAATAG AGGAAAAACCAT ATTTGGAGAACCA GCACAACATAG GAAAACCAT ATTTGGAGAACCA CTCACAGCTG ATCCACACCAG GCAGACACATG AGGGAGACACAT AACCTGGAACACATA GCAAAAACCAT ATTTGAGAGAACT (7566) AGGCAGACCC CACCCACACAACATG GAAAACCCA CTCACAGCTA AACCTGAACACATG ATCCACCACCATG GAGGAACCCC (7566) ACCTGCAGAGA CACCCTGAAGT CAGAGAGTTCA AGCCCACCATG AGGGACCCC GACGAGAGTG CAGAGACACATG CAGACACATG GAGAAACCCC (7566) ACCTGCACCACC ACCCTGAAGA AACTGGGACA AACCTGGACACATG GAGAAACCCC (7566) ACCTCCACCAC ACCCTGAAGA AACTGCGACA AACCTGGACACATG GAGAAACACACATACATAC AAAAAAAAAA						6676
TARACATGTGA CTTTCCAGAA TGAGTTCTGC TATGAAAAT GAAGCTAATT ATCCTTCTAT 6856 ATTTCTACC CTTTGTAAAT TATGATAATAT TTTAATCC TACTTGTTATT TGTGCTGATC CTTAGCCTAA GTCTTAGACA CAAGCTTCAG CTTCCAGTTG ATGTATGTTA TTTTAATGT 6976 TAATCTAATT GAATAAAAGT TATGAGATCA CTTGCAGTTG ATGTATGTATA TTTTAATGT 7036 AGCCAGGTAT AAAGTATTC TGGCCTCTAC TTTTTCTCA TTATTCTCCA TTAATTCTCA 7036 AGCCAGGTAT AAAGTATTC TGGCCTCTAC TTTTTCTCA TTATTCTCCA TTAATTATTCT 7096 CTATTATTTT TCTCTATTTC CTCCATTATT GTTAGATAAA CCACAATTAA CTAATGCTAC 7156 AGACTGAGCA CATAAGAGTA GCCAGGAGTG CTTACAAAATT GGCAATGCTA CTAATAGCTAC 7156 TCCACCAGTC CCCACTGAAA GACAGTTAGG TATGACAAATT GGCAATGCTA CAGAGGAGAA 7216 CCACCAGTC CCCACTGAAA GACAGTTAGG ATATGACCTA ATAAATATCC GCTTTCATGC 7276 CCACCAGTC CCCACTGAAA GACAGTTAGG ATATGACCTA ACTAAGACAC CTCACAGGGCA 7336 ACCTTGGTAGG GAGAAAAAG CCACCTCTAAA ATATAACCA ACTAAGGACA GTGCCACCC 7396 AACAGATACA GCCCCCAGAC AAATCCCTCA GCTATCCC TCCAACCAGA GTGCCACCC 7396 ACACATAATTA GAAGGAAG AGATGGCAA GCTCACACG GCACCTC TAACCAAGAGGC CCCACAGAGGGCA AAATCCCTCA GCTACACCAG GCACCTATACC ACCACATAATTA GAAGGAAAACG CCCCAGACA AACCCCTATCTA GACCTGACG GCACCTTTACTGAAAAT 7516 CCATAAGAGG CCTGGGATGG AAGCGTGAGA GCTCAAACCAT TCTGGGATAG GTGCAACCC 7576 AACATAATTA GAAGGAAGA AAACTGGGAT AAGCTGAACCTA TCTGGGATAG GTACCACCC 7564 AGCCAGAATCC GCAGATTCAG AAACTGGGAT AAGCCTGAACCT AGCACCTA TATGGAAACCT 75696 AGCCAAAATCC TATTGGGGA GACTGGCAAC GCTCAAACCTA TCTGGGATAG AGAAAACC 7636 AGCCACAACTA GCCCCAACACTA CCTGGGATGC ATTCTTGAACACT 75696 AGCAAAACCA TATTGGGGA GACCTGAAGT CAGGAGTTCA ACCCTGAACT TATTCAAAATA 7816 AAAAAAAAAA ATTAGCGGG TGGCCTCAAC CCTGTAATCC CAGCACACATG GGAGAACCC 7566 ACCACTCTAC AAAACAAA ATTAGCTGG CGTGGGGGG GAAGACCC CTGAGGCT ACCCGAGAGA ACCCACACACATG GAGAAACCC 7536 ACCTCTACTAC AAAACAAA ATTAGCTGG CGCGGAGG CAACCCC TGAGG CAGAACCC CTGAGG CAGAACCC CTGAGG CAGAACCC CTGAGG CAGAACCC CTGAGG CAGAACAC AACCCACCT GAGAAACCC CTGAGG CAGAACAC CTGAGGC AGCCACACCTG CAGAAACCC CTGAGG CAGAACAC CTGAGGAGAAACC CTGAGGAGAACA ACCCACACACAC CTGAGGC AGGAAACCC CTGAGAGAACA ACCCACACACAC CTGAGGCACC ACGAGGAGAA ACCCACACACAC CTGAGGCACC ACGCCACACCAC CTGAGGCACC A						6736
ATTCTAACAC CTTTGTAAAT TATGATAATA TTTTAATCC TAGTTGTTTT GTTGCTGATC CTTAGCCTAA GTCTTAGCCTAA GTCTTAGCCTAA GTCTTAGCCTAA GTCTTAGCCTAA GTCTTAGCCTAA GTCTTAGCCTAA GTCTAGCTAA GTCTTAGCAC CTCCAGTTG ATGATCATT ATTGTAATCT 6736 AGCCAGGTAT AAACTATTCT TGCCCTCTAC TTTTTCTCTA TTATTCTCCA TTATTTTTATCTCA TTATTTTTT TCTCTATTTC CTCCATTTAT GTTAGATAAA CACACATTAA CTTATATTCT 7096 AGACTAGCC AGTAAGAGTA GCCAGGGATG CTCACACATTAT GTAGATAAA CACACACTATAC CTATAGCTAC 7156 AGACTCAGC AGTAAGAGTA GCCAGGGATG CTTACAAATT GGCAATGCTT CACAGGGACA 7216 CTCACCCAGTC CCCACTGAAA GCCAGGTTAGG AGATTGCCA ATAAATATCC GCTTTCAGC 7376 AACAGAATACA GCCCCCAGGAC AATTCCCAA ATATCCAA ATAAATATCC GCTTTCAACC 7396 ACTTGGTAAGA GCCCCCCAGGA AATCCCTCAAA ATATAAATCCA AGTAAGAACA GTGCAACCCC 7336 ACTTGGTAACA GCCCCCCAGGA AATCCCCTCA GCTATCTCC TCCAACCACA GTGCCACCC 7366 ACACAGTAACA GCCCCCCAGAC AATCCCCTCA GCTATCTCC TCCAACCACA GTGCCACCC 7366 ACACATAACACA ATTTGGAAC 7664 AACACATAACA GCCCCCAGACA ACTCTAAA ATATAAATCCA AGTAAGAACA GTGCAACCC 7366 ACACATAACACA ATTTGGAACTTCA ACACATCACA GCCCCAACACA GCCCCCC AGACACACACACACA	ACAATCAGTC TTTATACA	AA TAATAATGTA	GAATACATAT	GTGAGTTATA	CATTTAAGAA	6796
TARTCTAATT GATTAAAAGT TATTGAGATCA GCTCTCAGTTG ATGTATGTTA TTTTTAATGT 7036 AGCCAGGTAT AAACTATTTC TATGGAGTCA GCTGTAAAAG TAATGCTATA ATTATCTTCA 7036 AGCCAGGTAT AAACTATTTC TGGCCTCTAC TTTTTCTCTA TTATTCTCCA TTATTATTCT 7096 CTATTATTTT TCTCTATTTC CTCCATTATT GTTAGATAAA CCACAATTAA CTATAGCTAC 7156 AGACTAGACC AGTAAAGAGTA GCCAGGGAG CTTACAAATT GGCAATGCAT CACAGGAGAA 7216 TCCCATCATCA TGAAGACTCT TTTTGAGTGA ACAAATT GGCAATGCAT CACAGGAGAA 7216 CCACCCAGTC CCCACTGAAA GCCAGGTGGAG GATACAAATT GGCAATGCAT CACAGGAGAA 7216 ACTTGGTAGG GAGAAAAAAG CCACTCTAAA ATATAATCC AGTGAAGGTC C736 AACAGATACA GCCCCCAGAC AAATCCCTCA GCTATCCC TCCAACAGA GTGCCACCC 7456 CTCAGGTGAC AATTTGGAGT CCCCATTCAA ATATAATCCA AGTAAGAACA GTGCACCCC 7456 CTCAGGTGAC AATTTGGAGT CCCCATTCAA GATACACAGA GTGCCACCC 7456 CTCAGGTGAC AATTTGGAGT CCCCATTCTA GACCTGACAG GCAGCTTAGT TATCAAAATA 7516 GCATAAGAGG CCTCGGATGA AAACTGGCCAA GCTCAACAGA GTGCCACCC 7456 ACACATAATTA GAAGGGAAG AAACTGGCCAA GCTCAACACTA TGTGGGATAG AGAAAACTC 7576 AGCATCAGAG GCACGATTCAA AAACTGGGAT AAGCCCTA TGTGGGATAG AGAAAACTC 7569 AGGGAGACTG GTGAAAATGT TAAGAAGAGT GAAATAATGC TTGTGGATAG AGTTCTTGTTG 7696 AGGGAGACTG GTGAAAATGT TAAGAAGATG GAAATAATGC TTGGCACTT TTTAAATTAA 7816 AAGAAATGT GCTGGGCGT GTGGCTCAA CCTGTAATC CACACACAT GTAGCACCC 77936 CTCGGGAGG TACCCTGAAGT TAATCAAAT TTTGATGGCC TTTTAAATTAA 7816 AAGAAATGT GCTGGCAG GAGAGTACA CCTGGAAC TTGTTAAATAA 7816 AAGAAATGT GAAAATACAAA ATTAGCTGG CTGGTGGCA TATGCCTGTA ATCCCAAGCTA 7936 CTCGGGAGG TGGCTGAAG AATTCTTTG AACCAGCCT GACCAACATC GAGAGACCCC 7936 CTCGGGAGG TGGCTGAAG AATTCTTTG AACCAGCCT GACCAACATC GAGAGACCCC 7936 CTCAGGCCAGA TGCCACTCC ACCTGGCCA AAACTCCC TTTTAAATAA 7816 AAAAAAAAAAAA AATAAAAA ATTAGCTTGG CTGGTGGCA TATGCCTGTA ATCCCAGCTA 7966 CTGGGCGGGG TGGCTGAAG AACTCTTTT AACTCAA AAAAAAAAAA	TAACATGTGA CTTTCCAG	AA TGAGTTCTGC	TATGAAGAAT	GAAGCTAATT	ATCCTTCTAT	6856
TAATCTAATT GAATAAAGT TATGAGATCA GCTGTAAAAG TAATGCTATA ATTATCTCA AGCCAGGTAT AAAGTATTTC TGCCTCTAC TTTTTCTCTA TTATTCTCAT TTAATTATCT 7096 CTATTATTTT TCTCTATTTC CTCCATTATT GTTAGATAAA CCACAATTAA CTATAGCTAC 7156 AGACTGAGCC AGTAAGAGTA GCCAGGGATG CTTACAAATT GCACAAATTAA CTATAGCTAC 7156 CTCCACCCAGTC CCCACTGAAA GCCAGGGATG CTTACAAATT GGCAATGCTT CAGAGGAGAA 7216 CCACCCAGTC CCCACTGAAA GACAGTTAG ATATGACCTT AGTGAAGAGTA CCAAGGAGAA 7216 CCACCCAGTC CCCCATGAAA GACAGTTAGA ATATAAATACCA GCTTTCATGC 7276 CCACCCAGTC CCCCCAGGA AAATCCCTCA GGTATCCCA ATAAAATACC GCTTTCATGC 7396 AACAGAATACA GCCCCCAGGA AAATCCCTCA GGTATCTCCC TCCAACCAGA GTGCCACCCC 7366 ACTTGGTAGG GAGAAAAAG CCACTCTAAA ATATAAATCCA AGTAAGAACA GTGCCACCCC 7456 TTCAGGTGAC AATTTGGAGT CCCCATTCTA GACCTGACAG GTGCCACCCC 7456 CCATAAGAGG CCCCCAGGCA AAATCCCCTCA GGTATCTCCC TCCAACCAGA GTGCCACCCC 7456 ACCTTAAAATATA GAAGGGAAGG AGATGGCCAA GCTCAAAGCTA TGTGGGATAAG AGGAAAAACT 7576 AGCGCAAAATCA AAACTGGGAT AAACTGGGAT AAGCTGAAGCTA TGTGGGATAAG AGGAAAACCT 7576 AGGGAGACTG GTGAAAATCT TAAGAAGAT GAAATAATAC TTTGGCACTTA GTAGAAACT 7756 AGGGAGACTG GTGAAAATCT TAAGAAGAT GAAATAATAC TTTGGCACTT GTAGAACCT 7756 AGGGGGGGAT CACCTGAAGT ATAGCACAC CTGTAATCC CAGCACTTT GGGAACCC 7756 ACTCTCACTA AAAATACAAAA ATTAGCTGGG CACACACACT GACCAACCCT GACCACCCT AGCACACCCT GACACACCCT ACCACACCCT CAAAAAAAA	ATTTCTACAC CTTTGTAA	AT TATGATAATA	TTTTAATCCC	TAGTTGTTTT	GTTGCTGATC	
AGCCAGGTAT AAAGTATTTC TGGCCTCTAC TTTTTCTCTA TTATTCTCA TTATATTCT 7096 CTATTATTTT TCTCTATTTC CTCCATTATT GTTAGATAAA CACACAATTAA CTATAGCTAC 7156 AGACTGAGCC AGTAACAGTA GCCAGGGAG CTTACAAATTA GGCAATCCT CAGAGGAGAA 7216 TTCCATCTA TGAAGAGTA GCCAGGGAG CTTACAAATTA GGCAATCCT CAGAGGAGAA 7216 CCACCCACC CCACTGAAA GACAGTTAGG AATTGCCA ATAAATATCC CCTTCCATCAAA ATAGACCTT AGTGAAGGACA CCACCAGC CCACTGAAA GACAGTTAGG ATATGACCTT AGTGAAGACA CCACCAGC CCACCAGAA GACAGTTAGA ATATAAATCCA AGTAAGAACA GTGCATCCC 7396 AACAGATACA GCCCCCAGAC AAATCCCTCA GCTATCTCC TCCAACCAGA GTGCCACCCC 7456 CTCAGCGGAC ATTTGGAGT CCCCATTCTA GACCTGACAG GCAGCTTAGT TATCAAAATA 7516 GCATAAGAGG CCTGGGATG AAGGGTAGG TGGAACAGG GCAGCTTAGT TATCAAAATA 7516 GCATAAGAG CCTGGGATG AAGGGTAGG TGGAACGGT TAGCACACAC GCAGCTTAGT TATCAAAAATA 7516 ACACTAAATAA GAAGGGAAG AAATCCCCAA GCTCAAAGCAT TGTGGGAATAC GTTACTCAAAAAACC 7576 AACATAATTA GAAGGGAAG AAACTGGCAA GCTCAAAGCTA TGTGGGAATAC GTTACTCAAAAACC 7576 AACAAATCCA TATTTGGGGG ACCTGAAGGT TATCAAAATT TTGATGGCACTTA GTAGAAACCC 7756 GGCAAAATCCA TATTTGGGGG ACCCTGAAGT TATCAAAATT TTGATGGCCC TTTTAAAAAAA 7816 AAAGAAATGG GCTGGAGG ACCCTGAAGT TATCAAATT TTGATGCCC TTTTAAAAAAA 7816 AAAGAAATGG GCTGGGCGG GCCCGAAGGT TATCAAATT TTGATGCCC TTTTAAAAAAA 7816 ACCCTCAAATCCA TATTTGGGGG GACCTGAAACCCC GACCAACATG GAGAAACCCC 7936 CTCGGGAGGC TGAGGCAGGA GAACCTTTTTG AACCCACACATG GAGAAACCCC 7936 CTCGGGAGGC TGAGGCAGGA GAACCTTTTTG AACCCACACATG GAGAAACCCC 7936 CTCGGGAGGC TGAGGCAGGA GAACCTTTTTG AACCCAGCTA ATCCCACGCTA ACCCAGCAC TATGCCACCAC TATGCCACCACACACGCA ACCCAGGAGG CACGAGAGCTG CACAACAGGC ATGCACCACAC TATGCCACCAC TATGCACCAC TATGCACCAC TATGCACCAC TATGCACCACAC TATGCACCAC TATGCACCAC TATGCACCAC TATGCACCAC TATGCACCAC TATACACAC TATACACACAC TATGCACCAC TATGCACACAC TATGCACAC TATGCACACAC TATGCACACAC TATGCACACAC TATGCACACAC TATCACACAC TATCACACA	CTTAGCCTAA GTCTTAGA	CA CAAGCTTCAG	CTTCCAGTTG	ATGTATGTTA	TTTTTAATGT	6976
CTATTATTTT TCTCTATTTC CTCCATTATT GTTAGATAAA CACACATTAA CTATAGCTAC 7156 AGGACTGAGCC AGTAAGAGTA GCCAGGGATG CTTACAAATT GGCAATGCTT CAGAGGAGA 7216 TTCCATCTCA TGAAGACTCT TTTTGACTGG AGATTTGCCA ATAAATTATC GCTTTCATGC CCACCCAGTC CCCACTGAAA GACAGTTTGG AGATTTGCCA ATAAATATCC GCTTTCATGC CACCCAGTC CCCACTGAAA GACAGTTTGG AGATTTGCCA ATAAATATCC GCTTTCATGC ACTTGGTAGG GAGAAAAAG CCACTCTAAA ATAAATACA AGTAAGAACA GTGCAATAGC AACAGATACA GCCCCCAGAC CAACTCTAA ATAAATACCA AGTAAGAACA GTGCAATAGC CCACTGGATGG CACCCCTAA ATAAATATCCA AGTAAGAACA GTGCAATAGC CCACTGGATGG CACCCCTAA ATAAATATCCA AGTACAAACA GTGCCACCCC TTCAAGGTGAC AATTTGGAGT CCCCATTCTA GACCTGACAG GCAGCTTAGT TATCAAAATA 7516 CCATAAGAGG CCTGGGATGG AAGGGTAGGG TGGAAAGGGT TAAGCAATAGT TATCAAAATA 7516 CCATAAGAGG CCTGGGATGG AGGGTAGGG TGGAAAGGGT TAAGCAATGCT GTTACTCAAAC AGCTGCAGAG GCAGATTCAG AAACTGGGAT AGGTCAGACG CTACAGGTGG ATTCTTTTTG 7576 AGCATAAATA GAAGGGAAGA AAACTGGGAT AGGTCGAAC CTACAAGGTGG ATTCTTTTTTG 7696 AGCAAATCA TATTTGGGGG AGCTGAAGT TAAGAAATATGC TTGGCACTTA GTAGGAACTG 7756 GGCAAATCCA TATTTGGGGC AGCCTGAAGT TAATTCAAATT TTGATGGCCC TTTTAAATAA 7816 AAAGAATGTG GCTGGCGTG GTGGCTCACA CCTGTAATCC CAGCCATTA GTAGGAACCC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGGG CGTGGTCACA CCTGTAATCC CAGCCATTA GACAACATG GAGAACCCC 7936 ATCTCTGACTA AAAATACAAA ATTAGCTGGG CGTGGTGCA TATGCCACTCT GACAACATG GAGAACCCC 7936 CTCGGGAGGC TGAGGCAGGA GAATCTTTT AGCTGGCA TATGCCACCT ACCAACATG GAGAACCCC 7936 ACCTCTGCAGGC TGAGGCAGGA GAATCTTTTT AGCTGGCA TTTTTTAAGTA 116 AAAAAAAAAAA TATACCA ACACTGGGCA ACAAGAGCAA AACTCGGTCT CAAAAAAAAAA						7036
AGACTGAGCC AGTAAGAGTA GCCAGGGATG CTTACAAATT GGCAATGCTT CAGAGGAGAA 7216 TTCCATGTCA TGAAGACTCT TTTTGAGTGG AGATTTGCCA ATAAATATCC GCTTTCATGC CCACCCAGTC CCACTGAAA GACAGTTAGG ATATGACCTT AGTGAAGAGTC CCAACGAGG CCCACCCAGGC CAAGGAGAAAAAG CCACTCTAAA ATATAATCCA AGTAAGACACT GTCCACCCAGC AACAGATACA GCCCCCAGAC AAATCCCTCA GCTATCTCC TCCAACCAGA GTGCCACCCC TTCAGGTAGA ATTTGGAGT CCCCATTCTA AGACTGACAG GCAGCTTAGT TATCAAAATA 7516 GCATAAGAGG CCTGGGATG AAGGGTAGG TGGAAAGGG CAACTAGT TATCAAAATA 7516 GCATAAGAG CCTGGGATG AAGGGTAGG TGGAAAGGG TATAGCATG TATCAAAATA 7516 GCATAAGAG CCTGGGATG AAGGGTAGG TGGAAAGGT TATTGAAAATA 7516 AACATAATTA GAAGGGAAG AGATGGCCAA GCTCAAGCTA TGTGGGATAG AGCAGACTCA GCAGATTCAG GAAAACTC 7636 AGCGGAGACTG GTGAAAATGT TAAGAAAGAT GAAAAAAAAAA	AGCCAGGTAT AAAGTATT	C TGGCCTCTAC	TTTTTCTCTA	TTATTCTCCA	TTATTATTCT	7096
TTCCATGTCA TGAAGACTCT TTTTGAGTG AGATTTGCCA ATAAATATCC GCTTTCATGC CACCCAGTC CCCACTGAAA ACACGTTAGG ATATGACCTT AGTGAAAGTA CAAGGGGCA 7336 ACTGGGTAGG GAAAAAAG CACCTCTAAA ATATAATCCA AGTGAAAGTAC GTGCATATGC 7396 AACAGATACA GCCCCCAGAC AAATCCCTCA GCTATCCC TCCAACCAGA GTGCCATATGC 7396 ACAGATACA GCCCCCAGAC AAATCCCTCA GCCATCTCC TCCAACCAGA GTGCCATATGC 7396 ACAGATACA CATTGGAT CCCCATTCTA GACCTGACAG GCAGCTTAGT TATCAAAATA 7516 GCATAAGAGG CCTGGGATGG AAGGGTAGGG TGGAAAGGGT TAAGCATGCT GTTACTGAAAC 7576 AACATAATTA GAAGGGAAG AGATGCCAA GCCACACCAG GCAGCTTAGT TATCAAAATA 7516 GCCATACAGAG GCAGATTCAA AAACTGGGAT AGAGCCAAC AGACCAGA GCAGAACCAC AACTGGAT AGAGGAACCC 7466 ACGTGCAACCAG GCAGATTCAA AAACTGGGAT AACTGGGAT AGGCACACCA AGACTCAA AACTGGGAT AGAGCAACCAC AACTGGAT TATCAAAATA 7516 GCCAAAATATT GAAGGGAAG GCAGAATCCA AAACTGGGAT AACTGGAC TATCTGTGGAACT 7576 AACGAAACCA TATTTGGGGG ACCCCAACAACT TATTCAAATT TTGGCACTTA GTACGAACTC 7756 GCCAAAATCCA TATTTGGGG GTGGCTCACA CCTGTAATCC CAGCACCTTG GGAGCCCGA 7876 GGGGCGGAG CACCTGGAACT TATTCAATT TTGACACTC CAGCACCTTT GAAGAACCC 7936 ATCTCTACTA AAAAAAAAAA ATTAGCTGG CGTGGTGGCA TATGCCCTTA ACCCAGCAC AACCCCC AGCCCTGAAGT ACCCCGAGAC CAGCACCTT GAAGAAACCC 7936 ATCTCTACTA AAAAAAAAAA ATTAGCTGG CGTGGGCA TATGCCTCT ACCCAGCAT ACCCCAGCAT ACCCCAGCAC ACCCTGGACA GAACCACCC AACCACACAC GAACACACAC ACCCCAGCAC ACCCCCAGACACACAC	CTATTATTTT TCTCTATT	C CTCCATTATT	GTTAGATAAA	CCACAATTAA	CTATAGCTAC	7156
TTCCATGTCA TGAAGACTCT TTTTGAGTGG AGATTTGCCA ATAAATATCC GCTTTCATGC CCACCAGTC CCCACTGAAA GACAGTTAGG ATATGACCTT AGTGAAGGTC CCCACTGAAA GACAGTTAGG ATATGACCTT AGTGAAGGTC AGTGAAGGTC CCACAGAC AAATCCCTCA GCCACTCTAAA ATATAATCCA AGTAAGAACA GTGCCATATGC TTCAGGTGAC AAATTGGAGT CCCCAGAC AAATCCCTCA GCCACACAG GTGCCATATGC TACAGAGTACA GCCCCCAGAC AAATCCCTCA GCCACACAGA GTGCCACCCC TACAG CCACAGAC AATTTGAGAC CCCCGAGAC AAATCCCTCA GCCACACAG GCAGCTTAGT TATCAAAATA 7516 CCATAAGAGG CCTGGGATGG AAGGGTAGGG TGGAAAAGCT TTAGGACTG TTACTGAAC AGAGGAAGC AAACTCCAA GCCTGACAGC TACAGACTG TTACTGAAAATC AGAGGAAGC AAACTCGACA GCCCCAGAC AAACTCCAA GCCTGACAGC TTACTGAC TTTCTGAAAATC AGAGGAACCC TTACAGGATC AGAGGAACCC TTACTGACC TTTTCTGCACTC GGCAAAATCT GGCAAAATCT TAAGAAGACG AGACTCAAAAAATC TAATTGGGGG AGCCTGAAAATC TAATTTGGGGG AGCCTGAAGT TAATTCAATT TTGATGGCC TTTTTAAAATAA TTTAGACTCC CAGCACACTT GGAGACACCC TTTTTAAAATAA TTTAGTGGCC TTTTTAAAATAA TTTAGTGGCC TTTTTAAAATAA TTTAGCACTC AGCAGGAGC AGACCACCTTT TTTTAAAATAA ATTAGCTGGC AGCAGAGA AAATAACAAA ATTAGCTGGC AGCAGGAG AGAACCCC AGCCTGGACAC ACAGGGGCA AAAAAAAAAA	AGACTGAGCC AGTAAGAG	TA GCCAGGGATG	CTTACAAATT	GGCAATGCTT	CAGAGGAGAA	7216
CCACCAGTC CCCACTGARA GACAGTTAGA TATAGACTT AGTGAAGGTA CCAAGGGGCA ACTTGGTAGG GAGAAAAAA CCACTCTAAA ATATAATCCA AGTAAGAACA GTGCATATC 7396 AACAGATACA GCCCCCAGAC AAATCCCTC GCTATCTCC TCCAACCACA GTGCCACCCC 7456 GCATATGGAGT CCCCATTCTA GACTAGACACA GTGCCACCCC 7456 GTCAGGTGACA AATTTGGAGT CCCCATTCTA GACTGACAG GCAGCTTAGT TATCAAAATA 7516 GCATAAGACA CCTTGGATGG AAGGGTAGG TGGAAAGGGT TAAGCATGCT GTTACTGAAC 7576 AACATAATTA GAAGGGAAGG AGATGGCCAA GCTCAACGTA TGTGGAGATA AGGAAAACTC 7636 AGCTGCAGAG GCAGATTCAG AACATGAATTA GAAGGGAAAGGG AGATGGCCAA GCTCAACCTA TGTGGGATAA AGGAAAACTC 7636 AGCTGCAGAG GCAGATTCAG AACATGAATGT GTAGAAATGT GTAGAAATGT GTAGAAATGT GTAGAAATGT TTAGGAGACTG GTGAAAAATGT AACATGAAGT GAGCAAAATGT GAGCAAATGT GAGCAAATGT GAGCAAATGT GAGCAAATGT GAGCAAATGT GAGCAAATGT GAGCAAATGT GAGCAACTG GAGCACGAG AGCCTGAAGT TTATTCAATT TTGGCACTTA GTAGGAACCC 7756 AGGGGGGGGA CACCAACATG GAGCACCTG AGCCTGAAGT TATTCTAATT TTGGACCTT AGAGAACCC 7756 AGGGGGGGGA CACCACAATG GAGAAACCC 7756 AGACAACTG CACCACACTT AAAAAAAAAA ATTAGCTGGG CGTGGTGGCA TATGCCTGAA TCCCAGCTA 7796 AGCCAGCACTT AGACACACTG GAGAAACCC 7936 AGATCTTCC ATTCCACCA ACCCTC AGCACACTT AGCTCAAAAAAAA ATTAGCTGGC CATTGCACACA ACCCGGCAG ACCAACATG GAGAAACCC 7936 AGATCTTCC ATTGCACCA AGCCTGGGA ACCAACATG GAGAACCCC 7936 AGATCTTCC ATTGCACCA ACCCTGGAA ACCCGGGAG CACAACATG CACAACATG CACAACATG ACCCGGAG ACCAACATG CACAACATG TTTTAAATAA TTTAATACTC TTTTTAAGATA 8116 AAAAAAAAAAA ACCCGGAGG AGACCAA ACCCGGAGG ACCAACATTA ACCCCACT TTCACACAC CACAACATTA ACCCCACT TTCACACAC CACAACATG TTCACACACA CACAACATG TTCACACACA CACAACATG TTCACACACA CACAACATAA ATATTAACTT GAGGGGGA ACCAACATTA ACCCCACACT TTCACACACA CACAACATAA ATATTAACTC TTTCACACACA	TTCCATGTCA TGAAGACT	CT TTTTGAGTGG	AGATTTGCCA	ATAAATATCC	GCTTTCATGC	7276
ACTGGTAGG GAGAAAAAG CCACTCTAAA ATATAATCCA AGTAAGACA GTGCATATGC 7396 AACAGATACA GCCCCCAGAC AAATCCCTCA GCTATCTCC TCCAACCAGA GTGCCACCCC 7456 CTCAGGTGAC AATTTGGAGT CCCCATTCTA GACCTGACAG GCAGCTTAGT TATCAAAAATA 7516 GCATAAGAGG CCTGGGATGG AAGGGTAGG TGGAAAGGT TAAGCATGA TATCAAAAATA 7516 ACACTAAATTA GAAGGGAAGG AGATGGCCAA GCTCAAGCTA TGTGGGATAG AGGAAAACTC 7636 AGGGAGACTG GTGAAAATGT TAAGAAGATG GAAATAATGC TGTGGGATAG AGGAAAACTC 7636 AGGGAGACTG GTGAAAATGT TAAGAAGATG GAAATAATGC GCACAAGCTA TATTTGGGGA GGCCTCACA CCACAGGTGG ATTCTTGTTG 7696 AGGGAGATCCA TATTTGGGGG AGCCTGAAGT TTATTCAATT TTGATGGCCC TTTTAAATAA 7816 GGCGAAATCCA TATTTGGGGG GTGGCTCACA CCTGTAATCC CGCCACTTTG GAGGCCCAG 7756 GGGGGCGGAT CACCTGAAGT CAGCGAGTTCA AGACCAGCCT GACCACTTG GAGGCCCAG 7876 GGGGGCGGAT CACCTGAAGT CAGCGGAGTTCA AGACCAGCCT GACCACTTG GAGGACCAC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGGG CGTGGTGCA ACACAGGGC GAGAGACCC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGGG CGTGGTGCA ACACAGGGC ATTGCCACTC AGCCTGGACA ACACAGGACCA ACCTGAACAT GAGACACCC 7936 AGACCGGGG TGGAGCAAGA AATCTTTT AACCAGGTA ACCCGGGAG GCAGAGGTTC CAAAAAAAAAA						7336
AACAGATACA GCCCCCAGAC AATTCCATCA GCTATCTCC TCCAACCAG GTGCCACCCC 7456 TTCAGGTGAC AATTTGGAGT CCCCATTCTA GACCTGACAG GCACCTTAGT TATCAAAATA 7516 GCATAAGAGG CCTGGGATGG AAGGGTAGGG TGGAAAGGGT TAGCATCAGT GTTACTGAAC 7576 AACATAATTA GAAGGAAGG AGATGGCCAA GCTCAAGCTA TGTGGGATAG AGGAAAACTC 7636 AGCTGCAGAG GCAGATTCAG AAACTGGGAT AAGTCCGAAC CTACAGGTG ATTCTTGTTG 7696 AGGCAGACTG GTGAAAATGT TAAGAAGAGT GAAATATAC TGGCACTTA GTAGGAACTC 7656 GGCAAATCCA TATTTGGGGG AGCCTGAAGT TATTCAATT TTGATGGCCC TTTTAAATAA 7816 AAAGAATGTG GCTGGGCGTG GTGGCTCACA CCTGTAATCC CAGCCACTTA GTAGGAACTC 7876 GGGGGCGGAT CACCTGAAGT CAGGAGTTCA AGCCCAGCCT GACCACACTG GAGAAACCCC 7876 ATCTCTACTA AAAATACAAA ATTAGCTGG CGTGGCCCAC CCTGAACC CACCACATG GAGAAACCCC 7876 ATCTCTACTA AAAATACAAA ATTAGCTGG CGTGGCCAC TATGCCTGTA ACCCAGCATA ACCCAGCATA ACCCAGCTA ACCCAGCATA GAAAAAAAAAA						7396
TTCAGGTGAC AATTGGAGT CCCCATTCTA GACCTGACAG GCAGCTTAGT TATCAAAATA 7516 GCATAAAGAGG CCTGGGATGG AAGGGTAAGG TGGAAAGGT TAAGCATGCT GTTACTGAAC 7576 AACCATAAATTA GAAGGGAAGG AGATGGCCAA GCTCAAGCTA TAAGCATGCT AGGAAAACTC 7636 AGCTGCAGAG GCAGATTCAG AAACTGGGAT AAGTCCGAAC CTACAGGTGG ATTCTTGTTG 7696 AGGGAGACTG GTGAAAATGT TAAGAAGATG GAAAATAATGC TTTGATGGACTT GTGAGAACTG 7756 GGCAAATCCA TATTTGGGGG AGCCTGAAGT TATTCAATT TTGATGGCCC TTTTAAAATAA 7816 AAAGAAATGT GCTGGGCGTG GTGGCTCACA CCTGTAATCC CAGCACTTTG GGAGGCCGAG 7876 GGGGGCGGAT CACCTGAAGT CAGGAGTTCA AGACCAGCCT GACCAACATG GAGAAACCCC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGGG CGTGGTGGCA TATGCCAGCTA ATCCCAGCTA 7996 ACTCGGGAGGC TGAGGCAGGA GAATCTTTTG AACCCGGGAG GAGAGGCTG CGAGAGACCCC 7936 ACTCTGAGGC ATTGCACTC AGCCTGGGCA ACAAGAGCAA AACTCGGTCT CAAAAAAAAA 8116 AAAAAAAAAAA TGAAAATTAAC CAAAGGCAAT AGCTTAATAA TTTATATCTG GAGGGCGGA 64 AAAAAAAAAAA TGCAAACTGC TCTGGAAGGA AACTCAGCTT TATTCCAGCTA 8236 CAGCATCATA GCAAATCTGC TCTGGAAGG AACTCAATAA ATATTAGTTG GAGGGGGGG GAGAGGGGA 6ACTCAGTATA ACCCAGCATT TAAGCATTTTAAAGTA 8236 CAGCATCATA GCAAATCTGC TCTGGAAGG AACTCAATAA ATATTAGTTG GAGGGGGGG GAGAGGGA 6ACTCAATAA ACCCAGCACT TTTAATCCCT TTTCCTCCCA 8256 CAGAGTGAGG GGTGGACTAG GACCAGTTTT AGCCCTTGCCT TTTAATCCCT TTTCCTCCCA 8256 CAGAGTGAGG GACAGTTTAAAAA GTGGCCCAGG TTTGAGACCT TTTCCTCCCA 8256 CAGAGCCAGGC ACAGTGGCT ATGCCTATAA TCCCAGCACT TTGGAGGGC AAGGCGAGAGA 7676 CCTCACTTGA GACCAGCAT TCAAGACCAG CCTGGCCACG ATGGCATAC TCAGATAA AACAAAAAT ACCAAAAAAT ACCAAGACCAG CCTGGCCACG ATGGCATAC TCAGCACT 8596 CCGACCACT GCACCACGC CTGGGCGACA GAATGAGCT TTGCTCCAAA AAAAAAAAAA						7456
GCATAAGAGG CCTGGGATG AAGGGTAGGG TGGAAAGGGT TAAGCATGCT GTTACTGAAC 7576 AACATAATTA GAAGGGAAGG AGATGGCCAA GCTCAAGCTA TGTGGGATAG AGGAAAACTC 7636 AGCTGCAGAG GCAGATTCAG AAACTGGGAT AAGTCCGAAC CTACAGGTGG ATTCTTGTG 7696 AGGGAGACTG GTGAAAATGT TAAGAAGATG GAAATAATGC TTGGCACTTA GTAGGAACTG 7756 GGCAAATCCA TATTTGGGGG AGCCTGAAGT TTATTCAATT TTGGTGGCC TTTTAAATAA 7816 AAAGAATGTG GCTGGCGTG GTGCCTCACA CCTGTAATC CAGCACTTTG GAGGCCGAG 7876 GGGGGCGGAT CACCTGAAGT CAGGAGTTCA AGACCAGCCT GACCAACATG GAGAAACCC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGGG CGTGGCCAA AGCCAGCCT GACCAACATG GAGAAACCC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGG CGTGGCCAA AACCCAGGAG GAAACCCC 7936 AGATCGTGC ATTGCACTC AGCCTGGGCA ACAAGACCA AACTCGGTC CAAAAAAAA 8116 AAAAAAAAAA TGAAAATTAAC CAAAGGCAT AGCCTGAAG AACTCAGTCT CAAAAAAAA 8116 AAAAAAAAAA TGAAAATCTC TACAAGGCAT AAGCCAGCT TAAGCACTT TAAGCTCAT AAGCCAGCAT TATTAATAA TTTAATACTG TTTTAAAGTA 8176 GGGCGGGGGG TGGCTGAAG AGACTCGTTA AAATAAATAA TTTAAATACTG TTTTAAAGTA 8176 ACACATCATA GCAAATCTC TTTCGGAAGG AACTCAATAA ATTATAATCTG TTTTAAAGTA 8236 CTAATAAAGGA TCTTAGCAGT GACCAGCTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCCA 8256 CTAATAAAGGA TCTTAGCAGT GACCAGCTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCCA 8356 CTAATAAAGAA TACCAAGACAA ACCCAGTTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCCA 8356 CTAATAAAGAA TACCAAGACAA ACCCAGTTTT AGCCCTTGTC TTTAAATCCT TTTCCTGCCA 8356 CTGAGCCAGGC ACAGGGAT TCAAGACCAG CCTGGCCAGC ATGGCGATAC TCTGTCTCTA 8536 CTGAGCCTGA GCACCAGCC TGGCCAGC ATGGCCTAGC TTTCACTTAA TACAAGACAA ACCCTGTAATA TCCCAGCACT TTGGAAGACA CCCTGTAATA TCCCAGCACT TTTGCTCAAA AAAAAAAAAA						7516
AACATAATTA GAAGGGAAGG AGATGGCCAA GCTCAAGCTA TGTGGGATAG AGGAAAACTC 7696 AGCTGCAGAGG GCAGATTCAG AAACTGGGAT AAGTCCGAAC CTACAGGTG ATTCTTGTTG 7696 AGGGAGACTG GTGGAAAATGT TAGAGAAGATG GAAATAATGC TTGGCACTTA GTAGGAACTG 7756 GCCAAATCCA TATTTGGGG AGCCTGAAGT TTATTCAATT TTGATGGCC TTTTAAATAA 7816 AAAGAATGTG GCTGGAGAT CAGGAGTTCA AGACCACCTTG GCAGACCTTTG GGAGGCCGAG 7876 GGGGGGGGT CACCTGAAGT CAGGAGTTCA AGACCACCTT GACCAACATG GAGAAACCC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGGG CGTGGTGGCA TATGCCTGTA ACCCAGCTA AGACCACCATG GACAACATG GAGAAACCC 7936 ACATCGTGC ATTGCACTC AGCCTGGGCA ACACGGCT ACAGAGGCTA ACACGGCTA ACACGGGGGG CAGAGGTTG CAAAAAAAAA ATTAGCTGGC ACACACACTG ACAACACACTG CAAAAAAAAAA						7576
AGCTGCAGAG GCAGATTCAG AAACTGGGAT AAGTCCGAAC CTACAGGTG ATTCTTGTTG 7756 AGGGACACTG GTGAAAATGT TAAGAAGATG GAAATAATGC TTGCACTTA GTAGGAACTG 7756 GGCAAATCCA TATTTGGGGG AGCCTGAAGT TTATTCAATT TTGATGGCC TTTTAAATAA 7816 AAAGAATGTG GCTGGGCGTG GTGGCTCACA CCTGTAATCC CAGCACTTTG GGAGGCCGAG 7876 GGGGGCGGAT CACCTGAAGT CAGGAGTTCA AGACCAGCCT GACCAACATG GAGAAACCCC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGGG CGTGGTGGCA TATGCCACTA ATCCCAGCTA 7996 CTCGGGAGGC TGAGGCAGGA GAATCTTTTG AACCCGGGAG GCAGAGGTTG CGATGAGCCT 8056 AGATCGTGCC ATTGCACTCC AGCCTGGCCA ACAAGAGCAA AACTCGGTCT CAAAAAAAAA 8116 AAAAAAAAAA TGAAATTAAC CAAAGGCATT AGCTTAATAA TTTAATACTG TTTTTAAGTA 8176 GGGCGGGGG TGGCTGGAAG AGATCTTTTT AACCCGGGAG ACTGACATT TAAGCTTCAT 8236 CAGACTCATA GCAAATCTGC TTCTGGAAGG AACTCAATAA ATTATACTG TTTTTAAGTA 8236 CAGACTGAGG GGTGGACTA GACCAGTTTT AGCCCTTGTC TAATATACTT TAAGCTTCAT 8236 CAGACTGAG GGTGGACTA GACCAGTTTT AGCCCTTGTC TTTAAATCCCT TTTCCTGCCA 8356 CTAAAAAAAAA TACAAAAATT ACCCAGTTTT AGCCCTTGCC ATGGCGATAC TTTCCTGCCA 8356 CTAAAAAAAAA TACAAAAATT AGCCCATATAA TCCCAGCACT TTTGAATAA TAAGAATACAA 8416 CTAAAAAAAAA TACAAAAATT AGCCCATATAA TCCCAGCACT TTGGGAAGG AACGCGAGTG 8476 CTCACACTG GACCAGGACT TCAAGACCAG CCTGGCCAGC TTGGGAGGC AAGGCGAGTG 8476 CTGAGCCAGG GCAGAGAGA TCGCTTAAAA CCAGGAGGT TAGGCGTAAC TCTGTCTCTA 8536 CTAAAAAAAAA TACAAAAATT AGCCAGCAC GCTGGCCAGC TTGGCGAAC ACGCGAGTG 8476 CTGAGCCCACT GCACTCCAG CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAA 8716 CTGCACCACT GCACTCCAG CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAA 8716 CTGTCAGAGT TCTCTCAAC TTTCCAGTGC ACTGCACT TTGCTCAAA AAAAGAAAAA 8716 CTGTCAGAGT TCCCTCAGAC TTTCCAGTGC ACTGAGACT TTGTCTCAAA AAAAAAAAA AAACAAAAAA GAACTAACAC GCTTCCAGC TTTCCAGTGC TTTCACTGTT TATACACT TATCAAGCTC 8896 TCCCTTGGAT CAGACTCCAC TTTCCAGTGC TTTCCAGTGC TTTCAACTTT TATCCAGGCT TTGCAACA TTTCCAGGCT TTGCAACA TTTCCAGGCT TTGCAACA TTTCCAGGCT TTGCAACA TTTCCAGGCT TTGCAACA TTTCCAGGCT TTGCAACACT TTGCAGACT TTGCAACACT TTGCAGACT TTGCAACACT TTGCAGACT TTGCAACACT TTGCAACACT TTGCAACACT TTGCAACACT TTCCAGGCT TTCCAAGACT TTGCAACACT TTGCAACACT TTCCAACT TTGCAACACT TTCCAAGACT TTCCAAGACT						7636
AGGGAGACTG GTGAAAATGT TAAGAAGATG GAAATAATGC TTGGCACTTA GTAGGAACTG GGCAAATCCA TATTTGGGGG AGCCTGAAGT TTATTCAATT TTGATGGCCC TTTTAAATAA 7816 AAAGAATGTG GCTGGGCGTG GTGGCTCACA CCTGTAATCC CAGCACTTTG GGAGGCCGAG 7876 GGGGGCGGAT CACCTGAAGT CAGGAGTTCA AGACCAGCCT GACCAACATG GAGAAACCCC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGGG CGTGGTGCA TATGCCTGTA ATCCCAGCTA 7996 CTCGGGAGGC TGAGGCAGGA GAATCTTTG AACCCGGGAG GCAGAGGTTG CGATGAGCCT 8056 AGATCGTGC ATTGCACTCC AGCCTGGCA ACAAGAGCAA AACTCGGTCT CAAAAAAAA 8116 GGGCGGGGG TGGCTGGAAG AGATCTGTT AAATGAGAGCAA TTTTAATACTG TTTTTAAGATA 8176 GGGCGGGGG TGGCTGGAAG AGATCTGTT AAATGAGGCAA TTTTAATACTG TTTTTAAGATA 8176 CAGCATCATA GCAAATCTGC TTCTGGAAGG AACTCAATAA ATATTAGTTG GAGGGGGGA 8296 GAGAGTGAGG GGTGGACTAG GACCAGTTTT AGCCCTTGTC TTTAATACCT TTTCTGCAA 8356 CTAAAAAAAAA TCTTAGCAGT GGTTATAAAA GTGGCCTAGG TTCTAGAATA TAAGGTACAA 8416 CAGGCCAGGC ACAGTGGCTC ATGCCATATAA TCCCAGCATT TTTCTGCAA 8356 CTAAAAAAAAA TACAAAAAATT AGCCCTATAAA TCCCAGCATT TTTCTGCAA 8416 CTAAAAAAAAA TACAAAAAATT AGCCCTATAAA TCCCAGCACT TTGGGAAGGC AAGGCGAGTG 8476 CTAAAAAAAAA TACAAAAAATT AGCCCTATAAA CCAGGAGGT TTGGGAAGGC AAGGCGAGTG 8476 CTGAAAAAAAATT AGCCAGGCAT GGTGGCATGC ACCTGCAACT CCAGCACT TTGGGAAGGC AAGGCGAGTG 856 CTGGCACCACT GCACTCCAGC CTGGGCGAC GAATGAGACT TCCGTAATC CCAGCTACTC 8596 CTGAGCCTGA GCCACCCCTA TCGGGCGAC GAATGAGACT TTGTCTCAAA AAAAGAAAAAA 8716 GATACAACAG GCTACCCTTA TGTGCTCACC TTTCACTGTT TAAGGCTTACC 8596 CTGCACCACT GCACTCCAGC CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAAA 8716 GATACAACAG CTTCTTCATA TATACATA TACATGTATA TATGTTTCT TGAGAGGTTA 8856 CTGCACCACT CCCTCAGAC TTTCCAGTG ACCTTGACA ACCTTAAAA AAAAAAAAA AAAAAAAAAA						7696
GGCAAATCCA TATTTGGGGG AGCCTGAAGT TTATTCAATT TTGATGGCCC TTTTAAATAA AAAGAATGTG GCTGGGCGGG GTGGCTCACA CCTGTAATCC CAGCACTTTG GGAGGCCGAG 7876 ATCTCTACTA AAAATACAAA ATTAGCTGG CGTGGTGCCA TATGCCTGTA ATCCCAGCTA 7996 CTCGGGAGGC TGAGGCAGGA GAATCTTTTG AACCCAGCCT GACCAACATG GAGAACCCC 7936 AGATCGTGCC ATGCACTC AGCCTGGCCA ACAAGAGCAA AACTCGGTTG CAAAAAAAAA 8116 AAAAAAAAAA TGAAAATTAAC CAAAGGCATT AGCTTAATAA TTTAATACTG TTTTTAAGTA 8176 CGGCGGGGGG TGGCTGGAA AGAATCTGT AAATGAGGGA ACTCAATAA TTTAATACTG TTTTTAAGTA 8236 CAGCATCATA GCAAATCTGC TCTTGGAAGG AACTCAATAA ATATTAGCTTG TAAGCTTCAT 8236 CAGCATCATA GCAAATCTGC TCTTGGAAGG AACTCAATAA ATATTAGCTT TAAGCTTCAT 8236 CAGAGTGAGG GGTGGACTA GACCAGTTT AGCCTTGTC TTTAATCCCT TTTCCTGCA 8356 CTAATAAGGA TCTTAACAAG GGTTATAAAA GTGGCCTAGG TTCTAGATAA TAAGAATACAA 8416 CAGGCCAGGC ACAGTGGCTC ATGCCATTA ACCCTATAA ATGCCTATAA TAAGAATACAA 8416 CAGGCCAGGC ACAGTGGCTC ATGCCATAA TCCCAGCACT TTGGGAGGGC AAGGCGAGTG 8476 TCTCACTTGA GATCAGAAAAATT AGCCAGGAGT GGTGGCAACA CCTGGCCAGC ATGCCTATAA ACCAGAGAGT TCCACAGCACT TTGGGAGGGC AAGGCGAGTG 8476 CTAAAAAAAAA TACAAAAAATT AGCCAGGCAT GGTGGCAACA ACCTGAATA TAAGAATACAA 8416 GATACAACAG GCTACCCTTA TGTGCTCACC TTTCACATTA TAGGCTTCAAA AAAAAAAAAA						7756
AAAGAATGTG GCTGGGCGTG GTGGCTCACA CCTGTAATCC CAGCACTTTG GGAGGCCGAG GGGGGGCGGAT CACCTGAAGT CAGGAGTTCA AGACCAGCCT GACCAACATG GAGAAACCCC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGGG CGTGGTGCA TATGCCTGTA ATCCCAGCTA 7996 CTCGGGAGGC TGAGGCAGGA GAATCTTTG AACCCGGGAG GCAGAGGTTG CGATGAGCCT 8056 AGATCGTGCC ATTGCACTCC AGCCTGGGCA ACAAGAGCAA AACTCGGTCT CAAAAAAAAA 8116 AAAAAAAAAA GTGGCTGGAAG AGATCTGTT AAATGAGGAA ATCTGACATT TATAATACTG TTTTTAAGTA 8176 GGGCGGGGGG TGGCTGGAAG AGATCTGTT AAATGAGGAA ATCTGACATT TAAGCTTCAT 8236 CAGCATCATA GCAAATCTGC TTCTGGAAGG AACTCAATAA ATATTAGTTG GAGGGGGGA 8296 GAGGGGGGG GGTGGACTAG GACCAGTTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCA 8356 CTAATAAGGA TCTTAGCAGT GGTTAAAAA GTGGCCTAGG TTCTAGATAA TAAGATACAA ATATCCCT TTTCCTGCCA 8356 CTAATAAAAAAAA TACAAAAATT AGCCCAGCACT TTGGGAGGGC AAGGCGAGTG 8476 TCTCACTTGA GACCAGGAGT TCAAGACCAG CCTGGCCAGC ATGGCGATAC TCTGTCTCTA 8536 CTGGACCACT GCACACACA ACACCAGT TTGGCAACA ACACCAGCACT TTGGCAACA AAAAAAAA ACCCAGGCAT GGTGGCATGC ACCTGTAATC CCAGCTACTC 8596 GTGAGCCCAGC GCACCACACACACACACACACACACACACA						7816
GGGGGCGGAT CACCTGAAGT CAGGAGTTCA AGACCAGCCT GACCAACATG GAGAAACCCC 7936 ATCTCTACTA AAAATACAAA ATTAGCTGG CGTGGTGGCA TATGCCTGTA ATCCCAGCTA 7996 CTCGGGAGGC TGAGGCAGG GAATCTTTTG AACCCGGGAG GCAGAGGTTG CGATGAGCCT 8056 AGATCGTGCC ATTGCACTCC AGCCTGGGCA ACACAGAGCAA AACTCGGTCT CAAAAAAAAA 8116 AAAAAAAAAG TGAAATTAAC CAAAGGCATT AGCTTAATAA TTTAATACTG TTTTTAAGTA 8176 GGGCGGGGGG TGGCTGGAAG AGATCTGTT AACTCAATAA ATATTAGTTG GAGGGGGGA 8296 CAGCATCATA GCAAATCTGC TTCTGGAAGG AACTCAATAA ATATTAGTTT GAGGGGGGA 8296 CTAATAAAGGA TCTTAGCAGT GGTTATAAAA GTGGCCTAGG TTCTAGATAA TAAGATACAA 8416 CAGGCCAGGC ACAGTGGCTC ATGCCTATAA TCCCAGCACT TTGGGAGGGC AAGGCGAGTG 8476 CTCACTTGA GATCAGGAGT TCAAAGACCAG CCTGGCCAGC ATGCCGATAC TCTGTCTCTA 8536 CTAAAAAAAA TACCAAAAAAT AGCCAGCAT GGTGGCCTAGG TTCTAGATAA TAAGATACAA 8416 CTAAAAAAAA TACCAAAAAAT AGCCAGCAT GGTGGCCAGC ATGCCGATAC TCTGTCTCTA 8536 CTGCACCACT GCACCACC CTGGGCGAC GAATGGCTAAT CCAGCTACTC 6GAGCGGGGA 8656 CTGCACCACT GCACTCCAGC CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAA 8716 GATACAACAG GCAAGAGAA TCGCTTGACA CCAGGAGGT TAGGCTGAG TGAGCCTGAG 8656 CTGCACCACT GCACCCCTTA TGTGCTCACC TTTCCACTGT GATTACTAC TATAAAGTCC 8776 TATAAAGTTC CTGTTCATA TATACACAT TACATGATT TATCCAGGCT TGAGGCTTA 8836 CTGCACGAGT TCCCTCAGC TTTCCAGTC ACCTTAGAT TATCCAGGCT TTGAGAGGTTA 8836 CTGCACGAGT TCCCTCAGAC TTTCCAGTGC ACCTTAATA TATCCAGGCT 8896 TCCCTGGATT CAGATCAAC CCCTTCTGAT TAAAAAAAA AAAAAAAAA AAAAAAAAA GAAAGAAA						7876
ATCTCTACTA AAAATACAAA ATTAGCTGGG CGTGGTGGCA TATGCCTGTA ATCCCAGCTA 7996 CTCGGGAGGC TGAGGCAGGA GAATCTTTTG AACCCGGGAG GCAGAGGTTG CGATGAGCCT 8056 AGATCGTGCC ATTGCACTCC AGCCTGGCCA ACAAGAGCAA AACTCGGTCT CAAAAAAAAA 8116 AGAAAAAAAAG TGAAATTAAC CAAAGGCATT AGCTTAATAA TTTAATACTG TTTTTAAGTA 8176 CAGCATCATA GCAAATCTGC TTCTGGAAGG AACTCAATAA ATATTAGTTG GAGGGGGGGA 8296 GAGAGTGAGG GGTGGACTAG GACCAGTTTT AGCCCTTGTC TTTAATCCT TTTCCTGCCA 8356 CTAATAAGGA TCTTAGCAGT GACCAGTTTT AGCCCTAGTC TTTAATACCT TTTCCTGCCA 8356 CTAATAAGGA TCTTAGCAGT GGTTATAAAA GTGGCCTAGG TTCTAGATAA TAAGATACAA 8416 CAGGCCAGGC ACAGTGCCTC ATGCCTATAA TCCCAGCACT TTGGGAGGC AAGGCGAGTG ATGCCTATAA TACAAAAAAA TACAAAAAAAT AGCACAGCAC						7936
CTCGGGAGGC TGAGGCAGGA GAATCTTTTG AACCCGGGAG GCAGAGGTTG CGATGAGCCT AGATCGTGCC ATTGCACTCC AGCCTGGCA ACAAGAGCAA AACTCGGTCT CAAAAAAAAA 8116 AAAAAAAAAA TGAAATTAAC CAAAGGCATT AGCTTAATAA TTTAATACTG TTTTTAAGTA 8176 GGGCGGGGG TGGCTGGAAG AGATCTGTGT AAATGAGGGA ATCTGACATT TAAGCTTCATT GAGAGTGAGG GGTGGACTAG GACCAGTTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCCA 8356 CTAATAAAGA TCTTAGCAGT GACCAGTTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCCA 8356 CTAATAAAGA TCTTAGCAGT GACCAGTTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCCA 8356 CTAAAAAAAAA TACAAAAATT AGCCCTATAA TCCCAGCACT TTGGGAGGGG AAGCCGAGTG 8476 CTGGACCACT GCACCAGT TCCAGACA CCAGGAGTG TAGGCTGAAA AAAAGAAAAAA AACACTAAAA TAGCCTACTC 8596 GTGAGCCTGA GCACACCTTA TGGGCGACA CAAGCGGAGTG TAGGCTGAAA AAAAAAAAAA						7996
AGATCGTGCC ATTGCACTCC AGCCTGGCA ACAAGAGCAA AACTCGGTCT CAAAAAAAAA 8116 AAAAAAAAAG TGAAATTAAC CAAAGGCATT AGCTTAATAA TTTAATACTG TTTTTAAGTA 8236 CAGCATCATA GCAAATCTGC TTCTGGAAGG AACTCAATAA ATATTAGTTG GAGGGGGGGA 8296 GAGAGTGAGG GGTGGACTAG GACCAGTTT AGCCCTTGTC TTTAATCCT TTTCCTGCCA 8356 CTAATAAAGA TCTTAGCAGT GGTTATAAAA GTGGCCTAGG TTCTAGATAA TAAAGATACAA 8416 CAGGCCAGGC ACAGTGGCTC ATGCCTATAA TCCCAGCACT TTGGGAGGC AAGGCGAGTG 8476 CTCTCACTTGA GATCAGGAGT TCAAGACCAG CCTGGCCAGC ATGGCGATAC TCTGTCTCA CTAAAAAAAA TACAAAAATT AGCCAGCACT GGTGGCATCC CCAGCACT CCAGCACT TTGTCTCAAA AAAAGAAAAA 8536 CTGACCACT GCACTCCAGC CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAAA 8716 GATACAACAG GCTACCCTTA TGTGCTCACC TTTCACTGTT GATTACTAC TATAAAGTCC 7TATAAAGTC TTTTGGTCAAA AACCTTGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA 8836 CTGTCAGAGT TCCCTCAGC CTGGCCGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA 8836 CTGTCAGAGT TCCCTCAGC CTTGCACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA 8836 CTGTCAGAGT TCCCTCAGC CTTGCACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA 8836 CTGTCAGAGT TCCCTCAGAC TTTCCAGTC ACATCATAA TACATGATAT TATGTATCTA TATCCAGGCT 8896 TCCCTGGATT CAGATTCAC ACCTTGATA TATGTATCTA TATCCAGGCT 8896 TCCCTGGATT CAGATTCACC AGGTGGGCT TTCCAAGTTG GGGGTTCTC 9076 AAGGTCATTG GGATTGCTT CACATCCATT TGCTATGTAC CTTCCCTATG ATGGCTGGAA 9196 ATGTGCAAAA AGGTGATTA AAGAGATTGC CTGTTTCACC TATCCACCT CTATTCTGAA 9196 ATGTGCAAAA AGGTGATTA AAGAGATTGC CTGTTTCACC TATCCACCT CTATTCTCA 9256						8056
AAAAAAAAG TGAAATTAAC CAAAGGCATT AGCTTAATAA TTTAATACTG TTTTTAAGTA 8236 GGGCGGGGG TGGCTGGAAG AGATCTGTGT AAATGAGGGA ATCTGACATT TAAGCTTCAT 8236 CAGCATCATA GCAAATCTGC TTCTGGAAGG AACTCAATAA ATATTAGTTG GAGGGGGGA 8296 GAGAGTGAGG GGTGGACTAG GACCAGTTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCCA 8356 CTAATAAGGA TCTTAGCAGT GGTTATAAAA GTGGCCTAGG TTCTAGATAA TAAGATACAA 4416 CAGGCCAGGC ACAGTGGCTC ATGCCTATAA TCCCAGCACT TTGGGAGGG AAGGCGAGTG ATGCCTATAA ACCAGTGCACAC ATGGCCATAC CCAGCACT TCTGTCTCTA AGCCCAGCACT TCTGTCTCTA AGCCCAGCACT TCTGTCTCTA AGCCCAGCACT GCACCACAC ACCTGTAATC CCAGCACTC CAGCCACAC ACCGCACAC TCTGCCACACAC TCTGCCACACAC TTGTCTCAAA AAAAAAAAAA						8116
GGGCGGGGG TGGCTGGAAG AGATCTGTT AAATGAGGGA ATCTGACATT TAAGCTTCAT 8236 CAGCATCATA GCAAATCTGC TTCTGGAAGG AACTCAATAA ATATTAGTTG GAGGGGGGA 8296 GAGAGTGAGG GGTGGACTAG GACCAGTTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCCA 8356 CTAATAAGGA TCTTAGCAGT GGTTATAAAA GTGGCCTAGG TTCTAGATAA TAAGATACAA 8416 CAGGCCAGGC ACAGTGGCTC ATGCCTATAA TCCCAGCACT TTGGGAGGGC AAGGCGAGTG TCAAAAAAAA TACAAAAAATT AGCCAGCACT GGTGGCAGCA ATGCCTATAA CCCAGCACT TTGGGAGGC ACCGCACT CTGAGAAAAAAA TACAAAAAATT AGCCAGGCAT GGTGGCATGC ACCTGTAAAC CCAGCACT GGAGCTGAGA GAATGAGACCA GAATGAGACT TTGTCTCAAA AAAAGAAAAA 8656 TCGCACCACT GCACTCCAGC CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAA 8716 GATACAACAG GCTACCCTTA TGTGCTCACC TTTCACTGTT GATTACTAGC TATAAAGTCC 8876 CTGTCAGAGT CTGTTTCATA TATATACATA TACATGTATA TATGTATCAT TATCCAGGCT 8896 TGGCCAGGGT TCCCTCAGAC TTTCCAGTC ACTTGGGAGA TGTTAGGTCA ATATCAACTT TGAGAGATTA TATGTATCTA TATCCAGGCT 8896 TCCCTGGATT CAGATCCACT CCCTTCTGAT GTAAAAAAAA AAAAAAAAAA						8176
CAGCATCATA GCAAATCTGC TTCTGGAAGG AACTCAATAA ATATTAGTTG GAGGGGGGA 8296 GAGAGTGAGG GGTGGACTAG GACCAGTTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCCA 8356 CTAATAAGGA TCTTAGCAGT GGTTATAAAA GTGGCCTAGG TTCTAGATAA TAAGATACAA 8416 CAGGCCAGGC ACAGTGGCTC ATGCCTATAA TCCCAGCACT TTGGGAGGGC AAGGCGAGTG 8476 TCTCACTTGA GATCAGGAGT TCAAGACCAG CCTGGCCAGC ATGGCGATAC TCTGTCTCTA 8536 CTAAAAAAAA TACAAAAATT AGCCAGGCAT GGTGGCATGC ACCTGTAATC CCAGCTACTC 8596 GTGAGCCTGA GGCAGAAGAA TCGCTTGAAA CCAGGAGGTG TAGGCTGCAG TGAGCTGAGA 8656 TCGCACCACT GCACTCCAGC CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAA 8716 GATACAACAG GCTACCTTA TGTGCTCACC TTTCACTGTT GATTACTAGC TATAAAGTCC 8776 TATAAAAGTTC TTTGGTCAAA AACCTTGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA TATATACATA TACATGTATA TATGTATCTA TATCCAGGCT 8896 CTGCCAGGGT TCCCTCAGAC TTTCCAGTGC ACTTGGGAGA TGTTAGGTCA ATATCAACTT 8896 TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAAA AAAAAAAAAA						8236
GAGAGTGAGG GGTGGACTAG GACCAGTTTT AGCCCTTGTC TTTAATCCCT TTTCCTGCCA CTAATAAGGA TCTTAGCAGT GGTTATAAAA GTGGCCTAGG TTCTAGATAA TAAGATACAA 8416 CAGGCCAGGC ACAGTGGCTC ATGCCTATAA TCCCAGCACT TTGGGAGGGC AAGGCGAGTG 8476 TCTCACTTGA GATCAGGAGT TCAAGACCAG CCTGGCCAGC ATGCCGATAC TCTGTCTCTA 8536 CTAAAAAAAA TACAAAAAATT AGCCAGGCAT GGTGGCATGC ACCTGTAATC CCAGCTACTC 8596 GTGAGCCTGA GGCAGAAGAA TCGCTTGAAA CCAGGAGGTG TAGGCTGCAG TGAGCTGAGA 8656 TCGCACCACT GCACCCCTTA TGTGCCACC TTTCACTGTT GATTACTAAA AAAAGAAAAA 8716 GATACAACAG GCTACCCTTA TGTGCCACC TTTCACTGTT GATTACTAC TATAAAGTTC TTTGGCAAGA AACCTTGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA TATCAAGAT TACCATGTAT TATGTATCTA TATCCAGGCT 8896 TCCCTGGATT CCCTCAGAC TTTCCAGTGC ACTTGGGAGA TGTTAGGTCA ATATCAACTT 8966 TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAAA AAAAAAAAAA						8296
CTAATAAGGA TCTTAGCAGT GGTTATAAAA GTGGCCTAGG TTCTAGATAA TAAGATACAA CAGGCCAGGC						8356
CAGGCCAGGC ACAGTGGCTC ATGCCTATAA TCCCAGCACT TTGGGAGGGC AAGGCGAGTG TCTCACTTGA GATCAGGAGT TCAAGACCAG CCTGGCCAGC ATGGCGATAC TCTGTCTCTA CTAAAAAAAA TACAAAAATT AGCCAGGCAT GGTGGCATGC ACCTGTAATC CCAGCTACTC GTGAGCCTGA GGCAGAAGAA TCGCTTGAAA CCAGGAGGTG TAGGCTGCAG TGAGCTGAGA TCGCACCACT GCACTCCAGC CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAA 8716 GATACAACAG GCTACCCTTA TGTGCTCACC TTTCACTGTT GATTACTAGC TATAAAGTCC TATAAAGTTC TTTGGTCAAG AACCTTGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA CTGTCAGAGT CTGTTTCATA TATATACATA TACATGTATA TATGTATCTA TATCCAGGCT TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAAA AAAAAAAAAA	CTAATAAGGA TCTTAGCA	T GGTTATAAAA	GTGGCCTAGG	TTCTAGATAA	TAAGATACAA	8416
TCTCACTTGA GATCAGGAGT TCAAGACCAG CCTGGCCAGC ATGGCGATAC TCTGTCTCTA 8536 CTAAAAAAAA TACAAAAATT AGCCAGGCAT GGTGGCATGC ACCTGTAATC CCAGCTACTC 8596 GTGAGCCTGA GGCAGAAGAA TCGCTTGAAA CCAGGAGGTG TAGGCTGCAG TGAGCTGAGA 8656 TCGCACCACT GCACTCCAGC CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAA 8716 GATACAACAG GCTACCCTTA TGTGCTCACC TTTCACTGTT GATTACTAGC TATAAAGTCC 7476 TATAAAGTTC TTTGGTCAAG AACCTTGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA 8836 CTGCCAGGGT TCCCTCAGAC TTTCCAGTGC ACTTGGGAGA TGTTAGGTCA ATATCAACTT 8956 TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAAA AAAAAAAAAA	CAGGCCAGGC ACAGTGGC	C ATGCCTATAA	TCCCAGCACT	TTGGGAGGGC	AAGGCGAGTG	8476
CTAAAAAAA TACAAAAATT AGCCAGGCAT GGTGGCATGC ACCTGTAATC CCAGCTACTC GTGAGCCTGA GGCAGAAGAA TCGCTTGAAA CCAGGAGGTG TAGGCTGCAG TGAGCTGAGA 8656 TCGCACCACT GCACTCCAGC CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAA 8716 GATACAACAG GCTACCCTTA TGTGCTCACC TTTCACTGTT GATTACTAGC TATAAAGTCC 8776 TATAAAGTTC TTTGGTCAAG AACCTTGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA 8836 CTGCCAGGGT TCCCTCAGAC TTTCCAGTGC ACTTGGGAGA TGTTAGGTCA ATATCAACTT 8956 TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAAA AAAAAAAAAA						8536
GTGAGCCTGA GGCAGAAGAA TCGCTTGAAA CCAGGAGGTG TAGGCTGCAG TGAGCTGAGA TCGCACCACT GCACTCCAGC CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAA 8716 GATACAACAG GCTACCCTTA TGTGCTCACC TTTCACTGTT GATTACTAGC TATAAAGTCC 8776 TATAAAGTTC TTTGGTCAAG AACCTTGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA 8836 CTGTCAGAGT CTGTTTCATA TATATACATA TACATGTATA TATGTATCTA TATCCAGGCT TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAAA AAAAAAAAAA	CTAAAAAAA TACAAAAA	T AGCCAGGCAT	GGTGGCATGC	ACCTGTAATC	CCAGCTACTC	8596
TCGCACCACT GCACTCCAGC CTGGGCGACA GAATGAGACT TTGTCTCAAA AAAAGAAAAA 8716 GATACAACAG GCTACCCTTA TGTGCTCACC TTTCACTGTT GATTACTAGC TATAAAGTCC 8776 TATAAAGTTC TTTGGTCAAG AACCTTGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA 8836 CTGTCAGAGT CTGTTTCATA TATATACATA TACATGTATA TATGTATCTA TATCCAGGCT 8896 TGGCCAGGGT TCCCTCAGAC TTTCCAGTGC ACTTGGGAGA TGTTAGGTCA ATATCAACTT 8956 CCTTTCCCCT TGGAGCACTC AAGTTTCACC AGGTGGGCT TTCCAAGTTG GGGGTTCTCC 9076 AAGGTCATTG GGATTGCTTT CACATCCATT TGCTATGTAC CTTCCCTATG ATGGCTGGA 9136 GTGGTCAACA TCAAAACTAG GAAAGCTACT GCCCAAGGAT GTCCTTACCT CTATTCTGAA 9196 ATGTGCAATA AGTGTGATTA AAGAGATTGC CTGTTCTACC TATCCACACT CTCGCTTTCA 9256	GTGAGCCTGA GGCAGAAG	AA TCGCTTGAAA	CCAGGAGGTG	TAGGCTGCAG	TGAGCTGAGA	8656
GATACAACAG GCTACCCTTA TGTGCTCACC TTTCACTGTT GATTACTAGC TATAAAGTCC TATAAAGTTC TTTGGTCAAG AACCTTGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA CTGTCAGAGT CTGTTTCATA TATATACATA TACATGTATA TATGTATCTA TATCCAGGCT TGGCCAGGGT TCCCTCAGAC TTTCCAGTGC ACTTGGGAGA TGTTAGGTCA ATATCAACTT TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAAA AAAAAAAAAA						8716
TATAAAGTTC TTTGGTCAAG AACCTTGACA ACACTAAGAG GGATTTGCTT TGAGAGGTTA CTGTCAGAGT CTGTTTCATA TATATACATA TACATGTATA TATGTATCTA TATCCAGGCT TGGCCAGGGT TCCCTCAGAC TTTCCAGTGC ACTTGGGAGA TGTTAGGTCA ATATCAACTT TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAAA AAAAAAAAAA						8776
CTGTCAGAGT CTGTTTCATA TATATACATA TACATGTATA TATGTATCTA TATCCAGGCT TGGCCAGGGT TCCCTCAGAC TTTCCAGTGC ACTTGGGAGA TGTTAGGTCA ATATCAACTT TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAAA AAAAAAAAA GAAAGAAATC CCTTTCCCCT TGGAGCACTC AAGTTTCACC AGGTGGGCT TTCCAAGTTG GGGGTTCTCC AAGGTCATTG GGATTGCTTT CACATCCATT TGCTATGTAC CTTCCCTATG ATGGCTGGA GTGGTCAACA TCAAAACTAG GAAAGCTACT GCCCAAGGAT GTCCTTACCT CTATTCTGAA ATGTGCAATA AGTGTGATTA AAGAGATTGC CTGTTCTACC TATCCACACT CTCGCTTTCA 9256	TATAAAGTTC TTTGGTCA	AG AACCTTGACA	ACACTAAGAG	GGATTTGCTT	TGAGAGGTTA	8836
TGGCCAGGGT TCCCTCAGAC TTTCCAGTGC ACTTGGGAGA TGTTAGGTCA ATATCAACTT TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAAA AAAAAAAAA GAAAGAAATC CCTTTCCCCT TGGAGCACTC AAGTTTCACC AGGTGGGCT TTCCAAGTTG GGGTTCTCC AAGGTCATTG GGATTGCTTT CACATCCATT TGCTATGTAC CTTCCCTATG ATGGCTGGGA GTGGTCAACA TCAAAACTAG GAAAGCTACT GCCCAAGGAT GTCCTTACCT CTATTCTGAA ATGTGCAATA AGTGTGATTA AAGAGATTGC CTGTTCTACC TATCCACACT CTCGCTTTCA 9256						8896
TCCCTGGATT CAGATTCAAC CCCTTCTGAT GTAAAAAAA AAAAAAAAA GAAAGAAATC 9016 CCTTTCCCCT TGGAGCACTC AAGTTTCACC AGGTGGGCT TTCCAAGTTG GGGGTTCTCC AAGGTCATTG GGATTGCTTT CACATCCATT TGCTATGTAC CTTCCCTATG ATGGCTGGA 9136 GTGGTCAACA TCAAAACTAG GAAAGCTACT GCCCAAGGAT GTCCTTACCT CTATTCTGAA 9196 ATGTGCAATA AGTGTGATTA AAGAGATTGC CTGTTCTACC TATCCACACT CTCGCTTTCA 9256						
CCTTTCCCCT TGGAGCACTC AAGTTTCACC AGGTGGGGCT TTCCAAGTTG GGGGTTCTCC 9076 AAGGTCATTG GGATTGCTTT CACATCCATT TGCTATGTAC CTTCCCTATG ATGGCTGGGA 9136 GTGGTCAACA TCAAAACTAG GAAAGCTACT GCCCAAGGAT GTCCTTACCT CTATTCTGAA 9196 ATGTGCAATA AGTGTGATTA AAGAGATTGC CTGTTCTACC TATCCACACT CTCGCTTTCA 9256	TCCCTGGATT CAGATTCA	AC CCCTTCTGAT	GTAAAAAAAA	AAAAAAAAA	GAAAGAAATC	
AAGGTCATTG GGATTGCTTT CACATCCATT TGCTATGTAC CTTCCCTATG ATGGCTGGGA 9136 GTGGTCAACA TCAAAACTAG GAAAGCTACT GCCCAAGGAT GTCCTTACCT CTATTCTGAA 9196 ATGTGCAATA AGTGTGATTA AAGAGATTGC CTGTTCTACC TATCCACACT CTCGCTTTCA 9256	CCTTTCCCCT TGGAGCAC	C AAGTTTCACC	AGGTGGGGCT	TTCCAAGTTG	GGGGTTCTCC	
GTGGTCAACA TCAAAACTAG GAAAGCTACT GCCCAAGGAT GTCCTTACCT CTATTCTGAA 9196 ATGTGCAATA AGTGTGATTA AAGAGATTGC CTGTTCTACC TATCCACACT CTCGCTTTCA 9256	AAGGTCATTG GGATTGCT	TT CACATCCATT	TGCTATGTAC	CTTCCCTATG	ATGGCTGGGA	
ATGTGCAATA AGTGTGATTA AAGAGATTGC CTGTTCTACC TATCCACACT CTCGCTTTCA 9256	GTGGTCAACA TCAAAACT.	AG GAAAGCTACT	GCCCAAGGAT	GTCCTTACCT	CTATTCTGAA	
ACTGTAACTT TCTTTTTTC TTTTTTCTT TTTTTCTTT TTTTTGAAAC GGAGTCTCGC 9316	ATGTGCAATA AGTGTGAT	TA AAGAGATTGC	CTGTTCTACC	TATCCACACT	CTCGCTTTCA	
	ACTGTAACTT TCTTTTTT	C TTTTTTTCTT	TTTTTCTTTT	TTTTTGAAAC	GGAGTCTCGC	9316



TCTGTCGCCC AGGCTAGAGT GCAGTGGCAC GATCTCAGCT CACTGCAAGC TCTGCCTCCC	9376
GGGTTCACGC CATTCTCCTG CCTCACCCTC CCAAGCAGCT GGGACTACAG GCGCCTGCCA	9436
CCATGCCCAG CTAATTTTTT GTATTTTTAG TAGAGACGGG GTTTCACCGT GTTAGCCAGG	9496
ATGGTCTCGA TCTCCTGAAC TTGTGATCCG CCCGCCTCAG CCTCCCAAAG TGCTGGGATT	9556
ACAGGCGTGA GCCATCGCAC CCGGCTCAAC TGTAACTTTC TATACTGGTT CATCTTCCCC	9616
TGTAATGTTA CTAGAGCTTT TGAAGTTTTG GCTATGGATT ATTTCTCATT TATACATTAG	9676
ATTTCAGATT AGTTCCAAAT TGATGCCCAC AGCTTAGGGT CTCTTCCTAA ATTGTATATT	9736
GTAGACAGCT GCAGAAGTGG GTGCCAATAG GGGAACTAGT TTATACTTTC ATCAACTTAG	9796
GACCCACACT TGTTGATAAA GAACAAAGGT CAAGAGTTAT GACTACTGAT TCCACAACTG	9856
ATTGAGAAGT TGGAGATAAC CCCGTGACCT CTGCCATCCA GAGTCTTTCA GGCATCTTTG	9916
AAGGATGAAG AAATGCTATT TTAATTTTGG AGGTTTCTCT ATCAGTGCTT AGGATCATGG	9976
GAATCTGTGC TGCCATGAGG CCAAAATTAA GTCCAAAACA TCTACTGGTT CCAGGATTAA	10036
CATGGAAGAA CCTTAGGTGG TGCCCACATG TTCTGATCCA TCCTGCAAAA TAGACATGCT	10096
GCACTAACAG GAAAAGTGCA GGCAGCACTA CCAGTTGGAT AACCTGCAAG ATTATAGTTT	10156
CAAGTAATCT AACCATTTCT CACAAGGCCC TATTCTGTGA CTGAAACATA CAAGAATCTG	10216
CATTTGGCCT TCTAAGGCAG GGCCCAGCCA AGGAGACCAT ATTCAGGACA GAAATTCAAG	10276
ACTACTATGG AACTGGAGTG CTTGGCAGGG AAGACAGAGT CAAGGACTGC CAACTGAGCC	10336
AATACAGCAG GCTTACACAG GAACCCAGGG CCTAGCCCTA CAACAATTAT TGGGTCTATT	10396
CACTGTAAGT TTTAATTTCA GGCTCCACTG AAAGAGTAAG CTAAGATTCC TGGCACTTTC	10456
TGTCTCTCT ACAGTTGGCT CAGAAATGAG AACTGGTCAG GCCAGGCATG GTGGCTTACA	10516
CCTGGAATCC CAGCACTTTG GGAGGCCGAA GTGGGAGGGT CACTTGAGGC CAGGAGTTCA	10576
GGACCAGCTT AGGCAACAAA GTGAGATACC CCCTGACCCC TTCTCTACAA AAATAAATTT	10636
TAAAAATTAG CCAAATGTGG TGGTGTATAC TTACAGTCCC AGCTACTCAG GAGGCTGAGG	10696
CAGGGGGATT GCTTGAGCCC AGGAATTCAA GGCTGCAGTG AGCTATGATT TCACCACTGC	10756
ACTTCTGGCT GGGCAACAGA GCGAGACCCT GTCTCAAAGC AAAAAGAAAA AGAAACTAGA	10816
ACTAGCCTAA GTTTGTGGGA GGAGGTCATC ATCGTCTTTA GCCGTGAATG GTTATTATAG	10876
AGGACAGAAA TTGACATTAG CCCAAAAAGC TTGTGGTCTT TGCTGGAACT CTACTTAATC	10936
TTGAGCAAAT GTGGACACCA CTCAATGGGA GAGGAGAGAA GTAAGCTGTT TGATGTATAG	10996
GGGAAAACTA GAGGCCTGGA ACTGAATATG CATCCCATGA CAGGGAGAAT AGGAGATTCG	11056
GAGTTAAGAA GGAGAGGAGG TCAGTACTGC TGTTCAGAGA TTTTTTTAT GTAACTCTTG	11116
AGAAGCAAAA CTACTTTTGT TCTGTTTGGT AATATACTTC AAAACAAACT TCATATATTC	11176
AAATTGTTCA TGTCCTGAAA TAATTAGGTA ATGTTTTTTT CTCTATAG GAA ATG AAT	11233
Glu Met Asn	11200
85	
CCT CCT GAT AAC ATC AAG GAT ACA AAA AGT GAC ATC ATA TTC TTT CAG	11281
Pro Pro Asp Asn Ile Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Glu	11201
90 95 100	
AGA AGT GTC CCA GGA CAT GAT AAT AAG ATG CAA TTT GAA TCT TCA TCA	11329
Arg Ser Val Pro Gly His Asp Asn Lys Met Gln Phe Glu Ser Ser	1102)
105 110 115	
TAC GAA GGA TAC TTT CTA GCT TGT GAA AAA GAG AGA GAC CTT TTT AAA	11377
	110//
Tyr Glu Gly Tyr Phe Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys 120 125 130 135	
W-V	11/25
CTC ATT TTG AAA AAA GAG GAT GAA TTG GGG GAT AGA TCT ATA ATG TTC	11425
Leu Ile Leu Lys Lys Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe	
140 145 150	11161
ACT GTT CAA AAC GAA GAC TAGCTATTAA AATTTCATGC C	11464
Thr Val Gln Asn Glu Asp	
155	

# (18) INFORMATION FOR SEQ ID NO: 18:

# (i)SEQUENCE CHARACTERISTICS:

- (A)LENGTH: 471 base pairs (B)TYPE: nucleic acid
- (C)STRANDEDNESS: double



(D)TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi)ORIGINAL SOURCE:

(A)ORGANISM: mouse
(G)CELL TYPE: liver

### (ix)FEATURE:

- (A)NAME/KEY: mat peptide
- (B)LOCATION: 1..471
- (C) IDENTIFICATION METHOD: S

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

								CGG Arg		48
								TTC Phe		96
								AGA Arg 45		144
								GTG Val		192
								AAC Asn		240
TCC								GAT Asp		288
				TTT				AAC Asn		336
			TCA					TGC Cys 125		384
		GCT						GAA Glu		432
	TCT		ATG Met		CTC					471

### (19) INFORMATION FOR SEQ ID NO: 19:

### (i) SEQUENCE CHARACTERISTICS:

- (A)LENGTH: 9 amino acids
- (B)TYPE: amino acid
- (D)TOPOLOGY: linear

# (ii)MOLECULE TYPE: peptide

(v)FRAGMENT TYPE: N-terminal fragment

### (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Asn Phe Gly Arg Leu His Cys Thr Thr 1 5

### (20) INFORMATION FOR SEQ ID NO: 20:

- (i) SEOUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile 40 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile 55 Ser Val Lys Ser Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile 70 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys 90 85 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys 105 110 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu 120 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu 135 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp 150

### (21) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:





Ser Val Lys Ser Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile 70 80 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys 85 90 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys 110 105 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu 120 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu 135 140 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp 150

### (22) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn 10 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp 25 30 20 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile 35 40 45 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile 55 Ser Val Lys Ser Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile 75 70 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys 90 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys 100 105 110 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Ser Glu 120 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu 135 140 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp 155 150

### (23) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:



Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Ser Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile 40 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile 55 Ser Val Lys Ser Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys 85 90 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys 100 105 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Ser Glu 120 115 125 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu 135 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp 150

### (24) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn 10 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp 25 Met Thr Asp Ser Asp Ser Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile 40 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile 55 Ser Val Lys Ser Glu Lys Ile Ser Thr Leu Ser Ser Glu Asn Lys Ile 70 75 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys 90 85 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys 100 105 Met Gln Phe Glu Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Ser Glu 115 120 125 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu 135 140 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp 150

### (25) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 157 amino acids



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(B) TYPE: amino acid
(D) TOPOLOGY: linear

# (ii) MOLECULE TYPE: peptide

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn 10 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp 25 Met Thr Asp Ser Asp Ser Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile Ser Val Lys Ser Glu Lys Ile Ser Thr Leu Ser Ala Glu Asn Lys Ile 70 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys 90 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys 105 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu 125 120 115 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu 140 135 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp

### (26) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: peptide

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn 10 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp 25 Met Thr Asp Ser Asp Ser Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile 40 45 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile Ser Val Lys Ser Glu Lys Ile Ser Thr Leu Ser Ala Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys 90 85 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys 110 105 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Ser Glu 120 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu

F

130 135 140 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp 145 150 155

### (27) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asn Phe Gly Arg Leu His Ala Thr Thr Ala Val Ile Arg Asn Ile Asn Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met 25 Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile 40 Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser **5**5 Val Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile 75 70 Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser 85 90 Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu 105 Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu 120 125 Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp 135 140 Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser 145 150

- (28) INFORMATION FOR SEQ ID NO: 28:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:





65					70					75					80
Ser	Phe	Glu	Glu	Met 85	Asp	Pro	Pro	Glu	Asn 90	Ile	Asp	Asp	Ile	Gln 95	Ser
Asp	Leu	Ile	Phe 100	Phe	Gln	Lys	Arg	Val 105	Pro	Gly	His	Asn	Lys 110	Met	Glu
Phe	Glu	Ser 115	Ser	Leu	Tyr	Glu	Gly 120	His	Phe	Leu	Ala	Ser 125	Gln	Lys	Glu
Asp	Asp 130	Ala	Phe	Lys	Leu	Ile 135	Leu	Lys	Lys	Lys	Asp 140	Glu	Asn	Gly	Asp
Lys 145	Ser	Val	Met	Phe	Thr 150	Leu	Thr	Asn	Leu	His 155	Gln	Ser			